



# 4

## SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.
  - (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF PATHOGENS
  - (iii) NUMBER OF SEQUENCES: 165
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: MEDLEN & CARROLL
    - (B) STREET: 220 MONTGOMERY STREET, SUITE 2200
    - (C) CITY: SAN FRANCISCO
    - (D) STATE: CALIFORNIA
    - (E) COUNTRY: UNITED STATES OF AMERICA
    - (F) ZIP: 94104
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: US
    - (B) FILING DATE:
    - (C) CLASSIFICATION:
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: CARROLL, PETER G.
    - (B) REGISTRATION NUMBER: 32,837
    - (C) REFERENCE/DOCKET NUMBER: FORS-01756
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (415) 705-8410
    - (B) TELEFAX: (415) 397-8338

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2506 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGGGGGA TGCTGCCCT CTGGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG	120
GTGCAGGCAG CGCAAGAGC CTCCCTCAAGG CCCTCAAGGA GGACGGGGAC	180
GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG	240

TACAAGGCAG	GCCGGGCCCC	CACGCCGGAG	GACTTCCCC	GGCAACTCGC	CCTCATCAAG	300
GAGCTGGTGG	ACCTCCTGGG	GCTGGCGCGC	CTCGAGGTCC	CGGGCTACGA	GGCGGACGAC	360
GTCCTGGCCA	GCCTGGCAA	GAAGGCGGAA	AAGGAGGGCT	ACGAGGTCCG	CATCCTCAC	420
GCCGACAAAG	ACCTTACCA	GCTCCTTCC	GACCGCATCC	ACGTCCCTCA	CCCCGAGGGG	480
TACCTCATCA	CCCCGGCCTG	GCTTTGGGAA	AAGTACGGCC	TGAGGCCCCA	CCAGTGGGCC	540
GACTACCAGG	CCCTGACCGG	GGACGAGTCC	GACAACCTTC	CCGGGGTCAA	GGGCATCGGG	600
GAGAAGACGG	CGAGGAAGCT	TCTGGAGGAG	TGGGGGAGCC	TGGAAGCCCT	CCTCAAGAAC	660
CTGGACCGGC	TGAAGCCCAG	CATCCGGAG	AAGATCCTGG	CCCACATGGA	CGATCTGAAG	720
CTCTCCTGGG	ACCTGGCAA	GGTGCGCACC	GACCTGCC	TGGAGGTGGA	CTTCGCCAAA	780
AGGCGGGAGC	CCGACCGGGA	GAGGCTTAGG	GCCTTCTGG	AGAGGCTTGA	GTTTGGCAGC	840
CTCCTCCACG	AGTTCGGCCT	TCTGGAAAGC	CCCAAGGCC	TGGAGGAGGC	CCCCTGGCCC	900
CCGCCGGAAG	GGGCCTTCGT	GGGCTTTGTG	CTTTCCCGCA	AGGAGCCAT	GTGGGCCGAT	960
CTTCTGGCCC	TGGCCGCC	CAGGGGGGGC	CGGGTCCACC	GGGCCCCCGA	GCCTTATAAA	1020
GCCCTCAGGG	ACCTGAAGGA	GGCGCGGGGG	CTTCTCGCA	AAGACCTGAG	CGTTCTGGCC	1080
CTGAGGGAAG	GCCTTGGCCT	CCCGCCCGGC	GACGACCCC	TGCTCCTCGC	CTACCTCCTG	1140
GACCCTTCCA	ACACCACCCC	CGAGGGGGTG	CCCCGGCGCT	ACGGCGGGGA	GTGGACGGAG	1200
GAGGCGGGGG	AGCGGGCCGC	CCTTCCGAG	AGGCTCTCG	CCAACCTGTG	GGGGAGGCTT	1260
GAGGGGGAGG	AGAGGCTCCT	TTGGCTTTAC	CGGGAGGTGG	AGAGGCCCCT	TTCCGCTGTC	1320
CTGGCCCACA	TGGAGGCCAC	GGGGGTGCGC	CTGGACGTGG	CCTATCTCAG	GGCCTGTCC	1380
CTGGAGGTGG	CCGAGGAGAT	CGCCCGCCTC	GAGGCCGAGG	TCTTCCGCCT	GGCCGGCCAC	1440
CCCTCAACC	TCAACTCCCG	GGACCAGCTG	GAAAGGGTCC	TCTTGACGA	GCTAGGGCTT	1500
CCCGCCATCG	GCAAGACGGA	GAAGACCGGC	AAGCGCTCCA	CCAGCGCCGC	CGTCCTGGAG	1560
GCCCTCCCG	AGGCCAACCC	CATCGTGGAG	AAGATCCTGC	AGTACCGGGA	GCTCACCAAG	1620
CTGAAGAGCA	CCTACATTGA	CCCCCTGCCG	GACCTCATCC	ACCCCAGGAC	GGGCCGCCTC	1680
CACACCGCT	TCAACCAGAC	GGCCACGGCC	ACGGGCAGGC	TAAGTAGCTC	CGATCCAAC	1740
CTCCAGAAC	TCCCCGTCCG	CACCCCGCTT	GGGCAGAGGA	TCCGCCGGGC	CTTCATCGCC	1800
GAGGAGGGT	GGCTATTGGT	GGCCCTGGAC	TATAGCAGA	TAGAGCTCAG	GGTGTGGCC	1860
CACCTCTCCG	GCGACGAGAA	CCTGATCCGG	GTCTTCAGG	AGGGCGGGGA	CATCCACACG	1920
GAGACCGCCA	GCTGGATGTT	CGCGTCCCC	CGGGAGGCCG	TGGACCCCT	GATGCCCGG	1980
CGGGCCAAGA	CCATCAACTT	CGGGGTCCCTC	TACGGCATGT	CGGCCACCG	CCTCTCCCAG	2040
GAGCTAGCCA	TCCCTTACGA	GGAGGCCAG	GCCTTCATTG	AGCGCTACTT	TCAGAGCTTC	2100

CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG	2160
GAGACCCCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG	2220
CGGGAGGCAG CCGAGCGCAT GCCCTTCAAC ATGCCGTCC AGGGCACCGC CGCCGACCTC	2280
ATGAAGCTGG CTATGGTAA GCTCTTCCCC AGGCTGGAGG AAATGGGGC CAGGATGCTC	2340
CTTCAGGTCC ACGACGAGCT GGTCTCGAG GCCCCAAAAG AGAGGGCGGA GGCGTGGCC	2400
CGGCTGGCCA AGGAGGTCA AGGAGGGGTG TATCCCCTGG CCGTGCCCC GGAGGTGGAG	2460
GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC	2506

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2496 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCGATGC TTCCCCCTTT TGAGCCCCAA GGCGCGGTGC TCCTGGTGGA CGGCCACAC	60
CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT	120
CAGGCGGTCT ACGGCTTCGC CAAAAGCCTC CTCAAGGCC TGAAGGAGGA CGGGGACGTG	180
GTGGTGGTGG TCTTGACGC CAAGGCCCCC TCCTTCCGCC ACAGGGCCTA CGAGGCCTAC	240
AAGGCGGGCC GGGCCCCCAC CCCGGAGGAC TTTCCCCGGC AGCTGGCCCT CATCAAGGAG	300
TTGGTGGACC TCCTAGGCCT TGTGCGGCTG GAGGTTCCCG GCTTGAGGC GGACGACGTG	360
CTGGCCACCC TGGCCAAGCG GGCGGAAAAG GAGGGTACG AGGTGCGCAT CCTCACTGCC	420
GACCGCGACC TCTACCAGCT CCTTCGGAG CGCATGCCA TCCTCCACCC TGAGGGGTAC	480
CTGATCACCC CGGCGTGGCT TTACGAGAAG TACGGCTGC GCCCGGAGCA GTGGGTGGAC	540
TACCGGGCCC TGGCGGGGGA CCCCTCGGAT AACATCCCCG GGGTGAAGGG CATCGGGAG	600
AAGACCGGCC AGAGGCTCAT CCGCGAGTGG GGGAGCCTGG AAAACCTCTT CCAGCACCTG	660
GACCAGGTGA AGCCCTCCTT GCAGGGAGAAG CTCCAGGCAG GCATGGAGGC CCTGGCCCTT	720
TCCCGGAAGC TTTCCAGGT GCACACTGAC CTGCCCTGG AGGTGGACTT CGGGAGGCAG	780
CGCACACCCA ACCTGGAGGG TCTGCGGGCT TTTTGAGC GGGTGGAGTT TGGAAAGCCTC	840
CTCCACGAGT TCGGCCTCCT GGAGGGGCCG AAGGCGCAG AGGAGGCCCT CTGGCCCCCT	900
CCGGAAGGGG CTTTTTGGG CTTTCCTTT TCCCGTCCCG AGCCCATGTG GGCGAGCTT	960
CTGGCCCTGG CTGGGGCGTG GGAGGGCGC CTCCATCGGG CACAAGACCC CCTTAGGGC	1020
CTGAGGGACC TTAAGGGGT GCGGGGAATC CTGGCCAAGG ACCTGGCGGT TTTGGCCCTG	1080

CGGGAGGGCC	TGGACCTCTT	CCCAGAGGAC	GACCCCATGC	TCCTGGCCTA	CCTTCTGGAC	1140
CCCTCCAACA	CCACCCCTGA	GGGGGTGGCC	CGGC GTTACG	GGGGGGAGTG	GACGGAGGAT	1200
GC GGGGGAGA	GGGCCCTCCT	GGCGAGCGC	CTCTTCCAGA	CCCTAAAGGA	GCGCCTTAAG	1260
GGAGAAGAAC	GCCTGCTTTG	GCTTTACGAG	GAGGTGGAGA	AGCCGTTTC	CCGGGTGTTG	1320
GCCCCGGATGG	AGGCCACGGG	GGTCCGGCTG	GACGTGGCCT	ACCTCCAGGC	CCTCTCCCTG	1380
GAGGTGGAGG	CGGAGGTGCG	CCAGCTGGAG	GAGGAGGTCT	TCCGCCTGGC	CGGCCACCCCC	1440
TTCAACCTCA	ACTCCCGCGA	CCAGCTGGAG	CGGGTGCTCT	TTGACGAGCT	GGGCCTGCCT	1500
GCCATCGGCA	AGACGGAGAA	GACGGGGAAA	CGCTCCACCA	GCGCTGCCGT	GCTGGAGGCC	1560
CTGCGAGAGG	CCCACCCCAT	CGTGGACCAC	ATCCTGCAGT	ACCGGGAGCT	CACCAAGCTC	1620
AAGAACACCT	ACATAGACCC	CCTGCCCGCC	CTGGTCCACC	CCAAGACCGG	CCGGCTCCAC	1680
ACCCGCTTCA	ACCAGACGGC	CACCGCCACG	GGCAGGCTTT	CCAGCTCCGA	CCCCAACCTG	1740
CAGAACATCC	CCGTGCGCAC	CCCTCTGGGC	CAGCGCATCC	GCCGAGCCTT	CGTGGCCGAG	1800
GAGGGCTGGG	TGCTGGTGGT	CTTGGACTAC	AGCCAGATTG	AGCTTCGGGT	CCTGGCCCAC	1860
CTCTCCGGGG	ACGAGAACCT	GATCCGGGTC	TTTCAGGAGG	GGAGGGACAT	CCACACCCAG	1920
ACCGCCAGCT	GGATGTCGG	CGTTTCCCCC	GAAGGGTAG	ACCCTCTGAT	GCGCCGGCG	1980
GCCAAGACCA	TCAACTTCGG	GGTGCTCTAC	GGCATGTCCG	CCCACCGCCT	CTCCGGGGAG	2040
CTTTCCATCC	CCTACGAGGA	GGCGGTGGCC	TTCATTGAGC	GCTACTTCCA	GAGCTACCCC	2100
AAGGTGCGGG	CCTGGATTGA	GGGGACCCCTC	GAGGAGGGCC	GCCGGCGGGG	GTATGTGGAG	2160
ACCCCTTTCG	GCCGCCGGCG	CTATGTGCC	GACCTCAACG	CCC GG GTGAA	GAGCGTGC	2220
GAGGC GGGCGG	AGCGCATGGC	CTTCAACATG	CCGGTCCAGG	GCACCGCCGC	CGACCTCATG	2280
AAGCTGGCCA	TGGTGC GGCT	TTTCCCCCGG	CTTCAGGAAC	TGGGGGCGAG	GATGCTTTG	2340
CAGGTGCACG	ACGAGCTGGT	CCTCGAGGCC	CCCAAGGACC	GGGCGGAGAG	GGTAGCCGCT	2400
TTGGCCAAGG	AGGTCA TGGA	GGGGGTCTGG	CCCCTGCAGG	TGCCCTGGA	GGTGGAGGTG	2460
GGCCTGGGGG	AGGACTGGCT	CTCCGCCAAG	GAGTAG			2496

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2504 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGGCAGA	TGCTTCGCT	CTTGAAACCC	AAAGGCCGGG	TCCTCCTGGT	GGACGGCCAC	60
CACCTGGCCT	ACCGCACCTT	CTTCGCCCTG	AAGGGCCTCA	CCACGAGCCG	GGCGAACCG	120
GTGCAGGCAGG	TCTACGGCTT	CGCCAAGAGC	CTCCTCAAGG	CCCTGAAGGA	GGACGGGTAC	180
AAGGCCGTCT	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGAG	240
GCCTACAAGG	CGGGGAGGGC	CCCGACCCCC	GAGGACTTCC	CCCAGCAGCT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGTTTACC	CGCCTCGAGG	TCCCCGGCTA	CGAGGCGGAC	360
GACGTTCTCG	CCACCCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GGTACGAGGT	GCGCATCCTC	420
ACCGCCGACC	GCGACCTCTA	CCAACCTCGTC	TCCGACCGCG	TCGCCGTCT	CCACCCCGAG	480
GGCCACCTCA	TCACCCCGGA	GTGGCTTGG	GAGAAGTACG	GCCTCAGGCC	GGAGCAGTGG	540
GTGGACTTCC	GCGCCCTCGT	GGGGGACCCC	TCCGACAACC	TCCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CCGCCCTCAA	GCTCCTCAAG	GAGTGGGGAA	GCCTGGAAAA	CCTCCTCAAG	660
AACCTGGACC	GGGTAAAGCC	AGAAAACGTC	CGGGAGAAGA	TCAAGGCCCA	CCTGGAAGAC	720
CTCAGGCTCT	CCTTGGAGCT	CTCCCGGGTG	CGCACCGACC	TCCCCCTGGA	GGTGGACCTC	780
GCCCAGGGGC	GGGAGCCCGA	CCGGGAGGGGG	CTTAGGGCCT	TCCTGGAGAG	GCTGGAGTTC	840
GGCAGCCTCC	TCCACGAGTT	CGGCCCTCCTG	GAGGCCCGCG	CCCCCTGGA	GGAGGCCCGCC	900
TGGCCCCCGC	CGGAAGGGGC	CTTCGTGGGC	TTCGTCCTCT	CCCGCCCCGA	GCCCATGTGG	960
GCGGAGCTTA	AAGCCCTGGC	CGCCTGCAGG	GACGGCCGGG	TGCACCGGGC	AGCAGACCCC	1020
TTGGCGGGGC	TAAAGGACCT	CAAGGAGGTC	CGGGGCCTCC	TCGCCAAGGA	CCTCGCCGTC	1080
TTGGCCTCGA	GGGAGGGCT	AGACCTCGTG	CCCGGGGACG	ACCCCATGCT	CCTCGCCCTAC	1140
CTCCTGGACC	CCTCCAACAC	CACCCCGAG	GGGGTGGCGC	GGCGCTACGG	GGGGGAGTGG	1200
ACGGAGGACG	CCGCCCACCG	GGCCCTCCTC	TCGGAGAGGC	TCCATCGGAA	CCTCCTTAAG	1260
CGCCTCGAGG	GGGAGGGAGAA	GCTCCTTGG	CTCTACCACG	AGGTGGAAAA	GCCCTCTCC	1320
CGGGTCCTGG	CCCACATGGA	GGCCACCGGG	GTACGGCTGG	ACGTGGCCTA	CCTTCAGGCC	1380
CTTCCCTGG	AGCTTGGGA	GGAGATCCGC	CGCCTCGAGG	AGGAGGTCTT	CCGCTTGGCG	1440
GGCCACCCCT	TCAACCTCAA	CTCCCGGGAC	CAGCTGGAAA	GGGTGCTCTT	TGACGAGCTT	1500
AGGCTTCCCG	CCTTGGGGAA	GACGCCAAAG	ACAGGCAAGC	GCTCCACCAAG	CGCCGCGGTG	1560
CTGGAGGCC	TACGGAGGC	CCACCCCATC	GTGGAGAAGA	TCCTCCAGCA	CGGGGAGCTC	1620
ACCAAGCTCA	AGAACACCTA	CGTGGACCCC	CTCCCAAGCC	TCGTCCACCC	GAGGACGGGC	1680
CGCCTCCACA	CCCGCTTCAA	CCAGACGGCC	ACGGCCACGG	GGAGGCTTAG	TAGCTCCGAC	1740
CCCAACCTGC	AGAACATCCC	CGTCCGCACC	CCCTTGGGCC	AGAGGATCCG	CGGGCCTTC	1800

GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCCGCTC	1860
CTCGCCCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC	1920
CACACCCAGA CCGCAAGCTG GATGTTCGGC GTCCCCCCCAG AGGCCGTGGA CCCCTGATG	1980
CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCCTACG GCATGTCCGC CCATAGGCTC	2040
TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA	2100
GCTTCCCCAA GGTGCGGGCC TGGATAGAAA AGACCCTGGA GGAGGGGAGG AAGCGGGGCT	2160
ACGTGGAAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA	2220
GCGTCAGGGA GGCGCGGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG	2280
ACCTCATGAA GCTGCCATG GTGAAGCTCT TCCCCCGCCT CCGGGAGATG GGGGCCCCGA	2340
TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCG CCAAGCGCGG GCCGAGGAGG	2400
TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG	2460
TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG	2504

(2) INFORMATION FOR SEO ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 832 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Arg	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
1				5					10					15	
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly
			20					25					30		
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
				35			40					45			
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	Val
				50			55				60				
Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly
				65			70			75				80	
Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu
				85				90					95		
Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	Glu
				100				105					110		
Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	Lys
				115				120					125		
Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	Asp
				130				135				140			

Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly  
 145 150 155 160  
 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro  
 165 170 175  
 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn  
 180 185 190  
 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu  
 195 200 205  
 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu  
 210 215 220  
 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys  
 225 230 235 240  
 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val  
 245 250 255  
 Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285  
 Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp  
 305 310 315 320  
 Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro  
 325 330 335  
 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu  
 405 410 415  
 Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg Glu  
 420 425 430  
 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala  
 450 455 460  
 Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr  
 530 535 540  
 Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 625 630 635 640  
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro  
 645 650 655  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 660 665 670  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685  
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 690 695 700  
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val  
 705 710 715 720  
 Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg  
 725 730 735  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 740 745 750  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
 755 760 765  
 Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His  
 770 775 780

Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala  
785 790 795 800

Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro  
805 810 815

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu  
820 825 830

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 831 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val  
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu  
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
35 40 45

Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Val Val Val Val Val  
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr  
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val  
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Arg Ala  
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu  
130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ala Ile Leu His Pro Glu Gly Tyr  
145 150 155 160

Leu Ile Thr Pro Ala Trp Leu Tyr Glu Lys Tyr Gly Leu Arg Pro Glu  
165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile  
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg  
195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys  
 210 215 220  
 Pro Ser Leu Arg Glu Lys Leu Gln Ala Gly Met Glu Ala Leu Ala Leu  
 225 230 235 240  
 Ser Arg Lys Leu Ser Gln Val His Thr Asp Leu Pro Leu Glu Val Asp  
 245 250 255  
 Phe Gly Arg Arg Arg Thr Pro Asn Leu Glu Gly Leu Arg Ala Phe Leu  
 260 265 270  
 Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu  
 275 280 285  
 Gly Pro Lys Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala  
 290 295 300  
 Phe Leu Gly Phe Ser Phe Ser Arg Pro Glu Pro Met Trp Ala Glu Leu  
 305 310 315 320  
 Leu Ala Leu Ala Gly Ala Trp Glu Gly Arg Leu His Arg Ala Gln Asp  
 325 330 335  
 Pro Leu Arg Gly Leu Arg Asp Leu Lys Gly Val Arg Gly Ile Leu Ala  
 340 345 350  
 Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Phe Pro  
 355 360 365  
 Glu Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr  
 370 375 380  
 Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp  
 385 390 395 400  
 Ala Gly Glu Arg Ala Leu Leu Ala Glu Arg Leu Phe Gln Thr Leu Lys  
 405 410 415  
 Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val  
 420 425 430  
 Glu Lys Pro Leu Ser Arg Val Leu Ala Arg Met Glu Ala Thr Gly Val  
 435 440 445  
 Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Glu Ala  
 450 455 460  
 Glu Val Arg Gln Leu Glu Glu Val Phe Arg Leu Ala Gly His Pro  
 465 470 475 480  
 Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu  
 485 490 495  
 Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser  
 500 505 510  
 Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val  
 515 520 525  
 Asp Arg Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr  
 530 535 540

Ile	Asp	Pro	Leu	Pro	Ala	Leu	Val	His	Pro	Lys	Thr	Gly	Arg	Leu	His
545									550						560
Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser
		565							570						575
Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg
			580						585						590
Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Val	Leu	Val	Val	Leu
			595				600					605			
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp
			610				615				620				
Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Gln
			625				630			635					640
Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Ser	Pro	Glu	Gly	Val	Asp	Pro	Leu
				645					650				655		
Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met
			660						665				670		
Ser	Ala	His	Arg	Leu	Ser	Gly	Glu	Leu	Ser	Ile	Pro	Tyr	Glu	Glu	Ala
			675					680				685			
Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Tyr	Pro	Lys	Val	Arg	Ala
			690				695				700				
Trp	Ile	Glu	Gly	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Gly	Tyr	Val	Glu	
			705				710			715			720		
Thr	Leu	Phe	Gly	:Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val
				725					730				735		
Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val
			740					745				750			
Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Arg	Leu	Phe
			755					760				765			
Pro	Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	Asp
			770				775				780				
Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Asp	Arg	Ala	Glu	Arg	Val	Ala	Ala
			785				790			795				800	
Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Trp	Pro	Leu	Gln	Val	Pro	Leu
				805					810				815		
Glu	Val	Glu	Val	Gly	Leu	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu	
			820					825				830			

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 834 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
1 5 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
20 25 30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg  
130 135 140

Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu  
145 150 155 160

Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu  
195 200 205

Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp  
225 230 235 240

Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu  
245 250 255

Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg  
260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
275 280 285

Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro  
290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp  
 305 310 315 320  
 Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg  
 325 330 335  
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350  
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
 355 360 365  
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380  
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400  
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415  
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430  
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445  
 Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460  
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg Leu Ala  
 465 470 475 480  
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495  
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly  
 500 505 510  
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
 515 520 525  
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
 530 535 540  
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
 545 550 555 560  
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575  
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590  
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
 595 600 605  
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620  
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
 625 630 635 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
 645 650 655  
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
 675 680 685  
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Gly Arg Lys Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn  
 725 730 735  
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
 755 760 765  
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
 770 775 780  
 Val His Asp Glu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
 785 790 795 800  
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala  
 805 810 815  
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala  
 820 825 830  
 Lys Gly

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGNNGGCGA TGCTTCCCC	TTTGAGCCC AAAGGCCGGG	TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT	CTTCGCCCTG AAGGGCCTCA	CCACCAGCCG GGGCGAACCG	120
GTGCAGGCAG	TCTACGGCTT CGCCAAGAGC	CTCCTCAAGG CCCTGAAGGA	180
NNGGCGGTGN	TGACGCCAAG GCCCCCTCCT	TCCGCCACGA GGCCTACGAG	240
GCCTACAAGG	CGGGCCGGGC CCCCACCCCG	GAGGACTTTC CCCGGCAGCT	300
AAGGAGCTGG	TGGACCTCCT GGGGCTTGCG	CGCCTCGAGG TCCCCGGCTA	360
		CGAGGCGGAC	

GACGTNCTGG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC	420
ACCGCCGACC GCGACCTCTA CCAGCTCCTT TCCGACCGCA TCGCCGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCCGGC GTGGCTTGG GAGAAGTACG GCCTGAGGCC GGAGCAGTGG	540
GTGGACTACC GGGCCCTGGC GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CCGCCCNAGA GCTCCTCNAG GAGTGGGGGA GCCTGGAAAA CCTCCTCAAG	660
AACCTGGACC GGGTGAAGCC CGCCNTCCGG GAGAAGATCC AGGCCCACAT GGANGACCTG	720
ANGCTCTCCT GGGAGCTNTC CCAGGTGCAC ACCGACCTGC CCCTGGAGGT GGACTTCGCC	780
AAGNGGCGGG AGCCCGACCG GGAGGGGCTT AGGGCCTTC TGAGAGGGCT GGAGTTTGGC	840
AGCCTCCTCC ACGAGTTCGG CCTCCTGGAG GGCCTCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGCCTT CGTGGGCTT GTCCTTCCC GCCCCGAGCC CATGTGGGCC	960
GAGCTTCTGG CCCTGGCCGC CGCCAGGGAG GGCCGGGTCC ACCGGGCACC AGACCCCTTT	1020
ANGGCCTNA GGGACCTNA GGAGGTGCAG GGNCTCCTCG CCAAGGACCT GGCGTTTG	1080
GCCCTGAGGG AGGGCCTNGA CCTCNTGCC GGGGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCCT CCAAACACCAC CCCCGAGGGG GTGGCCCGGC GCTACGGGGG GGAGTGGACG	1200
GAGGANGCGG GGGAGCGGGC CCTCCTNTCC GAGAGGCTCT TCCNGAACCT NNNGCAGCGC	1260
CTTGAGGGGG AGGAGAGGCT CCTTGAGGCTT TACCAGGAGG TGAGAGAACCC CCTTCCCCGG	1320
GTCCTGGCCC ACATGGAGGC CACGGGGTN CGGCTGGACG TGGCCTACCT CCAGGCCCTN	1380
TCCCTGGAGG TGGCGGAGGA GATCCGCCGC CTCGAGGAGG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TGCTCTTGA CGAGCTNGGG	1500
CTTCCCGCCA TCGGCAAGAC GGAGAAGACN GGCAAGCGCT CCACCAGCGC CGCCGTGCTG	1560
GAGGCCCTNC GNGAGGCCA CCCCATCGTG GAGAAGATCC TGCAAGTACCG GGAGCTCAC	1620
AAGCTCAAGA ACACCTACAT NGACCCCTG CCNGNCCTCG TCCACCCAG GACGGGCCGC	1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGCA GGCTTAGTAG CTCCGACCCC	1740
AACCTGCAGA ACATCCCCGT CCGCACCCCN CTGGGCCAGA GGATCCGCCG GGCCTCGTG	1800
GCCGAGGAGG GNTGGGTGTT GGTGGCCCTG GACTATAGCC AGATAGAGCT CGGGTCCTG	1860
GCCCACCTCT CGGGGGACGA GAACCTGATC CGGGTCTTCC AGGAGGGGAG GGACATCCAC	1920
ACCCAGACCG CCAGCTGGAT GTTCGGCGTC CCCCCGGAGG CCGTGGACCC CCTGATGCGC	1980
CGGGCGGCCA AGACCATCAA CTTCGGGGTC CTCTACGGCA TGTCCGCCA CGCCTCTCC	2040
CAGGAGCTG CCATCCCCTA CGAGGAGGCG GTGGCCTCA TTGAGCGCTA CTTCCAGAGC	2100
TTCCCCAAGG TGCAGGCCTG GATTGAGAAG ACCCTGGAGG AGGGCAGGAG GCGGGGGTAC	2160
GTGGAGACCC TCTTCGGCCG CGGGCGCTAC GTGCCCCGACC TCAACGCCCG GGTGAAGAGC	2220

GTGCGGGAGG CGGCGGAGCG CATGGCCTTC AACATGCCCG TCCAGGGCAC CGCCGCCGAC	2280
CTCATGAAGC TGGCCATGGT GAAGCTCTTC CCCC GGCTNC AGGAAATGGG GGCCAGGATG	2340
CTCCTNCAGG TCCACGACGA GCTGGTCCTC GAGGCCCCCA AAGAGCGGGC GGAGGNGGTG	2400
GCCGCTTTGG CCAAGGAGGT CATGGAGGGG GTCTATCCCC TGGCCGTGCC CCTGGAGGTG	2460
GAGGTGGGGA TGGGGGAGGA CTGGCTCTCC GCCAAGGAGT AG	2502

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 63
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 109
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 186
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 205
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 209
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 227..228
- (D) OTHER INFORMATION: /note= "Xaa at these positions can be any amino acid."

- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 233  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 240  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 243..244  
(D) OTHER INFORMATION: /note= "Xaa at these positions can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 247  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 260  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 290  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 329  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 336  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 340  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 368  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 414  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 417..418  
(D) OTHER INFORMATION: /note= "Xaa at these positions can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 431  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 551  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 605  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 773  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 794  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 798  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 823  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 833  
(D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Xaa Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
1 5 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
20 25 30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val  
50 55 60

Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala  
65 70 75 80

Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
85 90 95

Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu  
100 105 110

Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys  
115 120 125

Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp  
130 135 140

Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly  
145 150 155 160

Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro  
165 170 175

Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn  
180 185 190

Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu  
195 200 205

Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val  
210 215 220

Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa  
225 230 235 240

Leu Ser Xaa Xaa Leu Ser Xaa Val Arg Thr Asp Leu Pro Leu Glu Val  
245 250 255

Asp Phe Ala Xaa Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe  
260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
275 280 285

Glu Xaa Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
290 295 300

Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
305 310 315 320

Leu Leu Ala Leu Ala Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa  
 325 330 335  
 Asp Pro Leu Xaa Gly Leu Arg Asp Leu Lys Glu Val Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu  
 405 410 415  
 Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Ala  
 450 455 460  
 Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr  
 530 535 540  
 Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 625 630 635 640  
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro  
 645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 660 665 670  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685  
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 690 695 700  
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val  
 705 710 715 720  
 Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg  
 725 730 735  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 740 745 750  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
 755 760 765  
 Phe Pro Arg Leu Xaa Glu Met Gly Ala Arg Met Leu Leu Gln Val His  
 770 775 780  
 Asp Glu Leu Val Leu Glu Ala Pro Lys Xaa Arg Ala Glu Xaa Val Ala  
 785 790 795 800  
 Ala Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro  
 805 810 815  
 Leu Glu Val Glu Val Gly Xaa Gly Glu Asp Trp Leu Ser Ala Lys Glu  
 820 825 830  
 Xaa

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1647 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAATTCTGG	GGATGCTGCC	CCTCTTGAG	CCCAAGGGCC	GGGTCTCCT	GGTGGACGGC	60
CACCACCTGG	CCTACCGCAC	CTTCCACGCC	CTGAAGGGCC	TCACCACCAG	CCGGGGGGAG	120
CCGGTGCAGG	CGGTCTACGG	CTTCGCCAAG	AGCCTCCTCA	AGGCCCTCAA	GGAGGACGGG	180
GACGCGGTGA	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGGG	240
GGGTACAAGG	CGGGCCGGGC	CCCCACGCCG	GAGGACTTTC	CCCGGCAACT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCAGGCTA	CGAGGCGGAC	360
GACGTCTGG	CCAGCCTGGC	CAAGAAGGCG	AAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420

ACCGCCGACA AAGACCTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC CTGGCTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCAGGGT CAAGGGCATC	600
GGGGAGAAGA CGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC	780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTGGC	840
AGCCTCCTCC ACGAGTTCGG CCTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGCCTT CGTGGGCTTT GTGCTTCCC GCAAGGAGCC CATGTGGGCC	960
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCG CGAGCCTTAT	1020
AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTTCTCG CCAAAGACCT GAGCCTTCTG	1080
GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GGCGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCCTT CCAACACCAAC CCCCGAGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG	1200
GAGGAGGCGG GGGAGCGGGC CGCCCTTTCC GAGAGGCTCT TCGCCAACCT GTGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT CCTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTCCGCT	1320
GTCCTGGCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGGCCGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CGGGGACCAAG CTGGAAAGGG TCCTCTTGA CGAGCTAGGG	1500
CTTCCCGCCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCTG	1560
GAGGCCCTCC GCGAGGCCCA CCCCATCGTG GAGAAGATCC TGCAGGCATG CAAGCTTGGC	1620
ACTGGCCGTC GTTTTACAAC GTCGTGA	1647

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2088 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAATTCTGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCAACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAAG CGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG	240

GGGTACAAGG CGGGCCGGGC	CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT	GGGGCTGGCG CGCCTCGAGG TCCCAGGCTA CGAGGCGGAC	360
GACGTCCTGG CCAGCCTGGC	CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC	420
ACCGCCGACA AAGACCTTA	CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC	CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC	CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA	GCTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC	CGCCATCCGG GAGAAGATCC TGGCCCACAT GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC	780
AAAAGGCGGG AGCCCGACCG	GGAGAGGCTT AGGGCCTTTC TGAGAGGCT TGAGTTGGC	840
AGCCTCCTCC ACGAGTCGG	CCTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGGCCTT	CGTGGCTTT GTGCTTCCC GCAAGGAGCC CATGTGGGCC	960
GATCTTCTGG CCCTGGCCGC	CGCCAGGGGG GGCCGGGTCC ACCGGGCCCG CGAGCCTTAT	1020
AAAGCCCTCA GGGACCTGAA	GGAGGCGCGG GGGCTTCTCG CCAAAGACCT GAGCGTTCTG	1080
GCCCTGAGGG AAGGCCTTGG	CCTCCCGCCC GGCGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCTT CCAACACCAC	CCCCGAGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG	1200
GAGGAGGCGG GGGAGCGGGC	CGCCCTTTC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT	CCTTGGCTT TACCGGGAGG TGAGAGGCC CCTTCCGCT	1320
GTCCTGGCCC ACATGGAGGC	CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGGCGGGGA	GATCGCCCGC CTCGAGGCC AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC	CCGGGACCAG CTGGAAAGGG TCCTCTTGA CGAGCTAGGG	1500
CTTCCCGCCA TCGGCAAGAC	GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCCTG	1560
GAGGCCCTCC GCGAGGCCCA	CCCCATCGTG GAGAAGATCC TGCAAGTACCG GGAGCTCAC	1620
AAGCTGAAGA GCACCTACAT	TGACCCCTTG CGGACCTCA TCCACCCAG GACGGGCCGC	1680
CTCCACACCC GCTCAACCA	GACGGCCACG GCCACGGCA GGCTAAGTAG CTCCGATCCC	1740
AACCTCCAGA ACATCCCCGT	CCGCACCCCG CTTGGCAGA GGATCCGCCG GGCCTTCATC	1800
GCCGAGGAGG GGTGGCTATT	GGTGGCCCTG GACTATAGCC AGATAGAGCT CAGGGTGCTG	1860
GCCCACCTCT CGGGCGACGA	GAACCTGATC CGGGTCTTCC AGGAGGGCG GGACATCCAC	1920
ACGGAGACCG CCAGCTGGAT	GTTCGGCGTC CCCCAGGAGG CCGTGGACCC CCTGATGCGC	1980
CGGGCGGCCA AGACCATCAA	CTTCGGGTC CTCTACGGCA TGTCGGCCCA CGCCTCTCC	2040
CAGGAGCTAG CTAGCCATCC	CTTACGAGGA GGCCCAGGCC TTCATTGA	2088

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 962 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAATTCTGG GGATGCTGCC CCTCTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCAACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAAG CGGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG	240
GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC	360
GACGTCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC	420
ACCGCCGACA AAGACCTTTA CCAGCTTCTT TCCGACCGCA TCCACGTCTT CCACCCCGAG	480
GGGTACCTCA TCACCCCCGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGCCCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC	780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTGGC	840
AGCCTCCTCC ACGAGTTCTGG CCTTCTGGAA AGCCCCAAGT CATGGAGGGG GTGTATCCCC	900
TGGCCGTGCC CCTGGAGGTG GAGGTGGGGAGA TAGGGGAGGA CTGGCTCTCC GCCAAGGAGT	960
GA	962

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1600 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGAATTCTG	GGGATGCTGC	CCCTCTTGA	GCCCAAGGGC	CGGGTCCTCC	TGGTGGACGG	60
CCACCACCTG	GCCTACCGCA	CCTTCCACGC	CCTGAAGGGC	CTCACCAACCA	GCCGGGGGGA	120
GCCGGTGCAG	GCGGTCTACG	GCTTCGCCAA	GAGCCTCCTC	AAGGCCCTCA	AGGAGGACGG	180
GGACGCGGTG	ATCGTGGTCT	TTGACGCCAA	GGCCCCCTCC	TTCCGCCACG	AGGCCTACGG	240
GGGGTACAAG	GCAGGGCCGGG	CCCCCACGCC	GGAGGACTTT	CCCCGGCAAC	TCGCCCTCAT	300
CAAGGAGCTG	GTGGACCTCC	TGGGGCTGGC	GCGCCTCGAG	GTCCCCGGGCT	ACGAGGCGGA	360
CGACGTCCTG	GCCAGCCTGG	CCAAGAAGGC	GGAAAAGGAG	GGCTACGAGG	TCCGCATCCT	420
CACCGCCGAC	AAAGACCTTT	ACCAAGCTCCT	TTCCGACCGC	ATCCACGTCC	TCCACCCGA	480
GGGGTACCTC	ATCACCCCCG	CCTGGCTTTG	GGAAAAGTAC	GGCCTGAGGC	CCGACCAGTG	540
GGCCGACTAC	CGGGCCCTGA	CCGGGGACGA	GTCCGACAAC	CTTCCCGGGG	TCAAGGGCAT	600
CGGGGAGAAG	ACGGCGAGGA	AGCTTCTGGA	GGAGTGGGGG	AGCCTGGAAG	CCCTCCTCAA	660
GAACCTGGAC	CGGCTGAAGC	CCGCCATCCG	GGAGAAAGATC	CTGGCCCACA	TGGACGATCT	720
GAAGCTCTCC	TGGGACCTGG	CCAAGGTGCG	CACCGACCTG	CCCCTGGAGG	TGGACTTCGC	780
CAAAAGGCGG	GAGCCGACC	GGGAGAGGCT	TAGGGCCTTT	CTGGAGAGGC	TTGAGTTGG	840
CAGCCTCCTC	CACGAGTTCG	GCCTTCTGGA	AAGCCCCAAG	ATCCGCCGGG	CCTTCATCGC	900
CGAGGGAGGG	TGGCTATTGG	TGGCCCTGGA	CTATAGCCAG	ATAGAGCTCA	GGGTGCTGGC	960
CCACCTCTCC	GGCGACGAGA	ACCTGATCCG	GGTCTTCCAG	GAGGGGCGGG	ACATCCACAC	1020
GGAGACCGCC	AGCTGGATGT	TCGGCGTCCC	CCGGGAGGCC	GTGGACCCCC	TGATGCGCCG	1080
GGCGGCCAAG	ACCATCAACT	TCGGGGTCCT	CTACGGCATG	TCGGCCCACC	GCCTCTCCCA	1140
GGAGCTAGCC	ATCCCTTACG	AGGAGGCCA	GGCCTTCATT	GAGCGCTACT	TTCAGAGCTT	1200
CCCCAAGGTG	CGGGCCTGGA	TTGAGAAGAC	CCTGGAGGAG	GGCAGGAGGC	GGGGTACGT	1260
GGAGACCTC	TTCGGCCGCC	GCCGCTACGT	GCCAGACCTA	GAGGCCCGGG	TGAAGAGCGT	1320
CGGGGAGGCG	GCCGAGCGCA	TGGCCTTCAA	CATGCCCGTC	CGGGGCACCG	CCGCCGACCT	1380
CATGAAGCTG	GCTATGGTGA	AGCTCTTCCC	CAGGCTGGAG	GAAATGGGGG	CCAGGATGCT	1440
CCTTCAGGTC	CACGACGAGC	TGGCCTCGA	GGCCCCAAAA	GAGAGGGCGG	AGGCCGTGGC	1500
CCGGCTGGCC	AAGGAGGTCA	TGGAGGGGGT	GTATCCCTG	GCCGTGCC	TGGAGGTGGA	1560
GGTGGGGATA	GGGGAGGACT	GGCTCTCCGC	CAAGGAGTGA			1600

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACGAATTCTG GGGATGCTGC CCCTCTTGAA GCCCAA

36

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTGAGATCTA TCACTCCTTG GCGGAGAGCC AGTC

34

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 91 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAATACGACT CACTATAGGG AGACCGGAAT TCGAGCTCGC CCGGGCGAGC TCGAATTCCG

60

TGTATTCTAT AGTGTACCT AAATCGAATT C

91

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGATT TAGGTGACAC TATAGAA

27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTAATCATGG TCATAGCTGG TAGCTTGCTA C

31

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATCCTCTA GAGTCGACCT GCAGGCATGC CTACCTTGGT AG

42

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATCCTCTA GAGTCGACCT GCAGGCATGC

30

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2502 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAATTCTGG GGATGCTGCC CCTCTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAAG CGGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG	240
GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCAGGCTA CGAGGCGGAC	360
GACGTCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATTCTC	420
ACCGCCGACA AAGACCTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCCTC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC	780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTGGC	840
AGCCTCCTCC ACGAGTCGG CCTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGCCTT CGTGGGCTTT GTGCTTCCC GCAAGGAGGCC CATGTGGGCC	960
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCG CGAGCCTTAT	1020
AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTTCTCG CCAAAGACCT GAGCGTTCTG	1080
GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GGCGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCTT CCAACACCCAC CCCCGAGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG	1200
GAGGAGGCGG GGGAGCGGGC CGCCCTTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT CCTTCTGGCTT TACCGGGAGG TGGAGAGGCC CCTTCCGCT	1320
GTCCTGGCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGGCCGGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CGGGGACCAAG CTGGAAAGGG TCCTCTTGA CGAGCTAGGG	1500

CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCCTG	1560
GAGGCCCTCC	GCGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGTACCG	GGAGCTCACCC	1620
AAGCTGAAGA	GCACCTACAT	TGACCCCTTG	CCGGACCTCA	TCCACCCCCAG	GACGGGCCGC	1680
CTCCACACCC	GCTTCAACCA	GACGGCCACG	GCCACGGCA	GGCTAAGTAG	CTCCGATCCC	1740
AACCTCCAGA	ACATCCCCGT	CCGCACCCCG	CTTGGGCAGA	GGATCCGCCCG	GGCCTTCATC	1800
GCCGAGGAGG	GGTGGCTATT	GGTGGCCCTG	GAECTATAGCC	AGATAGAGCT	CAGGGTGCTG	1860
GCCCACCTCT	CCGGCGACGA	GAACCTGATC	CGGGTCTTCC	AGGAGGGGCG	GGACATCCAC	1920
ACGGAGACCG	CCAGCTGGAT	GTTCGGCCTC	CCCCGGGAGG	CCGTGGACCC	CCTGATGCGC	1980
CGGGCGGCCA	AGACCATCAA	CTTCGGGTC	CTCTACGGCA	TGTGGCCCA	CCGCCTCTCC	2040
CAGGAGCTAG	CCATCCCTTA	CGAGGAGGCC	CAGGCCTTCA	TTGAGCGCTA	CTTCAGAGC	2100
TTCCCCAAGG	TGCGGGCCTG	GATTGAGAAG	ACCCCTGGAGG	AGGGCAGGAG	GCGGGGGTAC	2160
GTGGAGACCC	TCTTCGGCCG	CCGCGCTAC	GTGCCAGACC	TAGAGGCCCG	GGTGAAGAGC	2220
GTGCGGGAGG	CGGCCGAGCG	CATGGCCTTC	AACATGCCCG	TCCGGGGCAC	CGCCGCCGAC	2280
CTCATGAAGC	TGGCTATGGT	GAAGCTCTTC	CCCAGGCTGG	AGGAAATGGG	GGCCAGGATG	2340
CTCCTTCAGG	TCCACGACGA	GCTGGTCCTC	GAGGCCCAA	AAGAGAGGGC	GGAGGCCGTG	2400
GCCCCGCTGG	CCAAGGAGGT	CATGGAGGGG	GTGTATCCCC	TGGCCGTGCC	CCTGGAGGTG	2460
GAGGTGGGGA	TAGGGAGGA	CTGGCTCTCC	GCCAAGGAGT	GA		2502

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATTAGGTG ACACATATA

19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 72 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGACGAACA AGCGAGACAG CGACACAGGT ACCACATGGT ACAAGAGGCA AGAGAGACGA 60  
CACAGCAGAA AC 72

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTTTCTGCTG TGTCGTCTCT CTTGCCTCTT GTACCATGTG GTACCTGTGT CGCTGTCTCG 60  
CTTGTTCGTC 70

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GACGAACAAG CGAGACAGCG 20

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTTTCTGCTG TGTCGTCTCT CTTG 24

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTTGTAC CATGTGGTAC CTGTGTCGCT GTCTCGCTTG TTCGTC

46

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACACAGGTAC CACATGGTAC AAGAGGCAAG AGAGACGACA CAGCAGAAAC

50

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTCGGGGAT GCTGCCCTC

60

TTTGAGCCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC

120

CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGGCGGT CTACGGCTTC

180

GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC

240

GCCAAGGCC CCTCCTTCCG CCACGAGGCC TACGGGGGT ACAAGGCGGG CCGGGCCCCC

300

ACGCCGGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGA CCTCCTGGGG

360

CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG

420

AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTTACCAG

480

CTTCTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG

540

CTTTGGGAAA	AGTACGGCCT	GAGGCCGAC	CAGTGGCCG	ACTACCGGGC	CCTGACCGGG	600
GACGAGTCCG	ACAACCTTC	CGGGGTCAAG	GGCATCGGGG	AGAAGACGGC	GAGGAAGCTT	660
CTGGAGGAGT	GGGGGAGCCT	GGAAGCCCTC	CTCAAGAAC	TGGACCGGCT	GAAGCCCGCC	720
ATCCGGGAGA	AGATCCTGGC	CCACATGGAC	GATCTGAAGC	TCTCCTGGGA	CCTGGCCAAG	780
GTGCGCACCG	ACCTGCCCT	GGAGGTGGAC	TTCGCCAAAA	GGCGGGAGCC	CGACCGGGAG	840
AGGCTTAGGG	CCTTTCTGGA	GAGGCTTGAG	TTTGGCAGCC	TCCTCCACGA	GTTCGGCCTT	900
CTGGAAAGCC	CCAAGTCATG	GAGGGGGTGT	ATCCCCTGGC	CGTGCCCTG	GAGGTGGAGG	960
TGGGGATAG						969

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 948 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGCTAGCA	TGACTGGTGG	ACAGCAAATG	GGTCGGATCA	ATTCGGGGAT	GCTGCCCTC	60
TTTGAGCCA	AGGGCCGGGT	CCTCCTGGTG	GACGGCCACC	ACCTGGCCTA	CCGCACCTTC	120
CACGCCCTGA	AGGGCCTCAC	CACCAGCCGG	GGGGAGCCGG	TGCAGGCGGT	CTACGGCTTC	180
GCCAAGAGCC	TCCTCAAGGC	CCTCAAGGAG	GACGGGGACG	CGGTGATCGT	GGTCTTGAC	240
GCCAAGGCC	CCTCCTTCCG	CCACGAGGCC	TACGGGGGGT	ACAAGGCGGG	CCGGGCCCCC	300
ACGCCGGAGG	ACTTTCCCCG	GCAACTCGCC	CTCATCAAGG	AGCTGGTGGA	CCTCCTGGGG	360
CTGGCGCGCC	TCGAGGTCCC	GGGCTACGAG	GCGGACGACG	TCCTGGCCAG	CCTGGCCAAG	420
AAGGCGGAAA	AGGAGGGCTA	CGAGGTCCGC	ATCCTCACCG	CCGACAAAGA	CCTTIAACCAG	480
CTTCTTCCG	ACCGCATCCA	CGTCCTCCAC	CCCGAGGGGT	ACCTCATCAC	CCC GG CCTGG	540
CTTTGGGAAA	AGTACGGCCT	GAGGCCGAC	CAGTGGCCG	ACTACCGGGC	CCTGACCGGG	600
GACGAGTCCG	ACAACCTTC	CGGGGTCAAG	GGCATCGGGG	AGAAGACGGC	GAGGAAGCTT	660
CTGGAGGAGT	GGGGGAGCCT	GGAAGCCCTC	CTCAAGAAC	TGGACCGGCT	GAAGCCCGCC	720
ATCCGGGAGA	AGATCCTGGC	CCACATGGAC	GATCTGAAGC	TCTCCTGGGA	CCTGGCCAAG	780
GTGCGCACCG	ACCTGCCCT	GGAGGTGGAC	TTCGCCAAAA	GGCGGGAGCC	CGACCGGGAG	840
AGGCTTAGGG	CCTTTCTGGA	GAGGCTTGAG	TTTGGCAGCC	TCCTCCACGA	GTTCGGCCTT	900
CTGGAAAGCC	CCAAGGCCGC	ACTCGAGCAC	CACCACCAACC	ACCAACTGA		948

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60
CACTATAGGG CGAACATTGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180
TTTCCTGTGT GAAATTGTTA TCCGCT	206

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTCTGGGTTTC TCTGCTCTCT GGTCGCTGTC TCGCTTGTTC GTC	43
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(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCTGTCTCGC TTGTTCGTC	19
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(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GACGAACAAG CGAGACAGCG

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCTGGGTTC TCTGCTCTCT GGTC

24

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GACGAACAAG CGAGACAGCG ACCAGAGAGC AGAGAACCCA GAA

43

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCAGAGAGC AGAGAACCCA GAA

23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACAGCTATG ACCATGATTA C

21

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CACCGTCCTC TTCAAGAAG	19
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(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTGAATCTTG TAGATAGCTA

20

(2) INFORMATION FOR SEQ ID NO:44

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCCTTATTAACTTTAAAAA TTTCAAAATG TTTCTTTAT ACACAATATG TTTCTTAGTC	60
TGAATAACCT TTTCCCTCTGC AGTATTTTG AGCAGTGGCT CCGAAGGCAC CGTCCTCTTC	120
AAGAAGTTA TCCAGAACGCC AATGCACCCA TTAGACATAA CCGGGAATCC TACATGGTTC	180
CTTTTATACC ACTGTACAGA AATGGTGATT TCTTTATTTC ATCCAAAGAT CTGGGCTATG	240
ACTATAGCTA TCTACAAGAT TCAGGTAAAG TTTACTTTCT TTCAGAGGAA TTGCTGAATC	300
TAGTGTACC AATTTATTAA GAGATAACAC AAAACTTTA	339

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCCTTATTAACTTTAAAAA T	21
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(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAAGTTTG TGTTATCTCA	20
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(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTCTGTAA CAGTGGTATA AAAGGAACCA TGTAGGATTG CCGGTTATGT CCAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 165 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGCGGATAAC AATTCACAC AGGAAACAGC TATGACCAGT ATTACGCCAA GCTATTTAGG	60
TGACACTATA GAATACTCAA GCTTGCATGC CTGCAGGTCG ACTCTAGAGG ATCCCCGGGT	120
ACCGAGCTCG AATTGCCCT ATAGTGAGTC GTATTAGGAT CCGTG	165

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT 60  
 CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT 120  
 GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG 180  
 TTTCTGTGT GAAATTGTTA TCCGCT 206

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGCGGATAAC AATTCACAC AGGA 24

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CACGGATCCT AATACGACTC ACTATAGGG 29

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CGCCAGGGTT TTCCCAGTCA CGAC 24

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGGAC CCATTAGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCA	157

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCA	157

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCA GACC CAGACTCTT TCAAGACTAC	180
ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GGCGCGATG	240
GTAGGGGCCG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG	300
AGAAAGCAGC TTCCTGAAGA AAAGCAGCCA CTCCTCATGG AGAAAGAGGA TTACCACAGC	360
TTGTATCAGA GCCATTAA	378

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTAT TTCATCCAAA	120
GATCTGGCT ATGACTATAG CTATCTACAA GATTCAAGACC CAGACTCTT TCAAGACTAC	180
ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTGG GGCAGCGATG	240
GTAGGGGCCG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG	300
AGAAAGCAGC TTCCTGAAGA AAAGCAGCCA CTCCTCATGG AGAAAGAGGA TTACCCACAGC	360
TTGTATCAGA GCCATTAA	378

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCAAGTTTGG CTTTTGGGAA CCAAACGTCA CAGAGAGACG ACTCTTGGTG AGAAGAAACA	60
TCTTCGATTT GAGTGCCCA GAGAAGGACA AATTTTTGC CTACCTCACT TTAGCAAAGC	120
ATACCATCAG CTCAGACTAT GTCATCCCCA TAGGGACCTA TGGCCAAATG AAAATGGAT	180
CAACACCCAT GTTTAACGAC ATCAATATTT ATGACCTCTT TGTCTGGATG CATTATTATG	240
TGTCAATGGA TGCAGTGCTT GGGGGATATG AAATCTGGAG AGACATTGAT TTTGCCATG	300
AAGCACCAAGC TTTTCTGCCT TGGCATAGAC TCTTCTTGTG GCGGTGGGAA CAAGAAATCC	360
AGAAGCTGAC AGGAGATGAA AACTTCACTA TTCCATATTG GGACTGGCGG GATGCAGAAA	420
AGTGTGACAT TTGCACAGAT GAGTACATGG GAGGTCAGCA CCCCACAAAT CCTAACTTAC	480
TCAGCCCAGC ATCATTCTTC TCCTCTTGGC AGATTGTCTG TAGCCGATTG GAGGAGTACA	540
ACAGCCATCA GTCTTTATGC AATGGAACGC CCGAGGGACC TTTACGGCGT AATCCTGGAA	600
ACCATGACAA ATCCAGAACCC CCAAGGCTCC CCTCTTCAGC TGATGTAGAA TTTTGCCTGA	660
GTGGACCCA ATATGAATCT GGTTCCATGG ATAAAGCTGC CAATTCAGC TTTAGAAATA	720
CACTGGAAGG ATTTGCTAGT CCACTTACTG GGATAGCGGA TGCCCTCTCAA AGCAGCATGC	780
ACAATGCCTT GCACATCTAT ATGAATGGAA CAATGTCCCA GGTACAGGGAA TCTGCCAACG	840
ATCCTATCTT CCTTCTTCAC CATGCATTG TTGACAGTAT TTTTGAGCAG TGGCTCCGAA	900
GGCACCGTCC TCTTCAAGAA GTTTATCCAG AAGCCAATGC ACCCATTGGA CATAACCGGG	960

AATCCTACAT GGTCCTTT ATACCACTGT ACAGAAATGG TGATTCTTT ATTCATCCA	1020
AAGATCTGGG CTATGACTAT AGCTATCTAC AAGATTCA	1059

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1059 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCAAGTTGG CTTTGGGA CCAAAGTGCA CAGAGAGACG ACTCTTGGTG AGAAGAAACA	60
TCTTCGATTT GAGTGCCCA GAGAAGGACA AATTTTTGC CTACCTCACT TTGCAAAGC	120
ATACCATCAG CTCAGACTAT GTCATCCCCA TAGGGACCTA TGGCAAATG AAAATGGAT	180
CAACACCCAT GTTTAACGAC ATCAATATTT ATGACCTCTT TGTCTGGATG CATTATTATG	240
TGTCAATGGA TGCAGTGCTT GGGGATATG AAATCTGGAG AGACATTGAT TTTGCCATG	300
AAGCACCGAC TTTCTGCCT TGGCATAGAC TCTTCTGTT GCGGTGGAA CAAGAAATCC	360
AGAAGCTGAC AGGAGATGAA AACCTCACTA TTCCATATTG GGACTGGCGG GATGCAGAAA	420
AGTGTGACAT TTGCACAGAT GAGTACATGG GAGGTCAGCA CCCCACAAAT CCTAACTTAC	480
TCAGCCCAGC ATCATTCTTC TCCTCTGGC AGATTGTCTG TAGCCGATTG GAGGAGTACA	540
ACAGCCATCA GTCTTATGC AATGGAACGC CCGAGGGACC TTTACGGCGT AATCCTGGAA	600
ACCATGACAA ATCCAGAACCC CCAAGGCTCC CCTCTTCAGC TGATGTAGAA TTTGCCTGA	660
GTTTGACCCA ATATGAATCT GGTTCCATGG ATAAAGCTGC CAATTCAGC TTTAGAAATA	720
CACTGGAAGG ATTTGCTAGT CCACTTACTG GGATAGCGGA TGCCTCTCAA AGCAGCATGC	780
ACAATGCCTT GCACATCTAT ATGAATGGAA CAATGTCCTA GGTACAGGGAA TCTGCCAACG	840
ATCCTATCTT CCTTCTTCAC CATGCATTG TTGACAGTAT TTTTGAGCAG TGGCTCCGAA	900
GGCACCGTCC TCTTCAAGAA GTTATCCAG AAGCCAATGC ACCCATTGGA CATAACCAGG	960
AATCCTACAT GGTCCTTT ATACCACTGT ACAGAAATGG TGATTCTTT ATTCATCCA	1020
AAGATCTGGG CTATGACTAT AGCTATCTAC AAGATTCA	1059

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1587 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGCTCCTGG	CTGTTTGTA	CTGCCTGCTG	TGGAGTTCC	AGACCTCCGC	TGGCCATTTC	60
CCTAGAGCCT	GTGTCTCCTC	TAAGAACCTG	ATGGAGAAGG	AATGCTGTCC	ACCGTGGAGC	120
GGGGACAGGA	GTCCCTGTGG	CCAGCTTCA	GGCAGAGGTT	CCTGTCAGAA	TATCCTTCTG	180
TCCAATGCAC	CACTTGGGCC	TCAATTCCC	TTCACAGGGG	TGGATGACCG	GGAGTCGTGG	240
CCTTCCGTCT	TTTATAATAG	GACCTGCCAG	TGCTCTGGCA	ACTTCATGGG	ATTCAACTGT	300
GGAAACTGCA	AGTTTGGCTT	TTGGGGACCA	AACTGCACAG	AGAGACGACT	CTTGGTGAGA	360
AGAAACATCT	TCGATTTGAG	TGCCCCAGAG	AAGGACAAAT	TTTTGCCTA	CCTCACTTTA	420
GCAAAGCATA	CCATCAGCTC	AGACTATGTC	ATCCCCATAG	GGACCTATGG	CCAAATGAAA	480
AATGGATCAA	CACCCATGTT	TAACGACATC	AATATTATG	ACCTCTTGT	CTGGATGCAT	540
TATTATGTGT	CAATGGATGC	ACTGCTTGGG	GGATATGAAA	TCTGGAGAGA	CATTGATTTT	600
GCCCATGAAG	CACCAGCTTT	TCTGCCTTGG	CATAGACTCT	TCTTGGTGC	GTGGGAACAA	660
GAAATCCAGA	AGCTGACAGG	AGATGAAAAC	TTCACTATTC	CATATTGGGA	CTGGCGGGAT	720
GCAGAAAAGT	GTGACATTTG	CACAGATGAG	TACATGGGAG	GTCAGCACCC	CACAAATCCT	780
AACTTACTCA	GCCCAGCATE	ATTCTTCTCC	TCTTGGCAGA	TTGTCTGTAG	CCGATTGGAG	840
GAGTACAACA	GCCATCAGTC	TTTATGCAAT	GGAACGCCCG	AGGGACCTTT	ACGGCGTAAT	900
CCTGGAAACC	ATGACAAATC	CAGAACCCCA	AGGCTCCCCT	CTTCAGCTGA	TGTAGAATT	960
TGCCTGAGTT	TGACCCAATA	TGAATCTGGT	TCCATGGATA	AAGCTGCCA	TTTCAGCTTT	1020
AGAAATACAC	TGGAAGGATT	TGCTAGTCCA	CTTAAGGGAA	TAGCGGATGC	CTCTCAAAGC	1080
AGCATGCACA	ATGCCTTGCA	CATCTATATG	AATGGAACAA	TGTCCCAGGT	ACAGGGATCT	1140
GCCAACGATC	CTATCTTCC	TCTTCACCAT	GCATTTGTTG	ACAGTATTTT	TGAGCAGTGG	1200
CTCCGAAGGC	ACCGTCCTCT	TCAAGAAGTT	TATCCAGAAG	CCAATGCACC	CATTGGACAT	1260
AACCGGGAAT	CCTACATGGT	TCCTTTATA	CCACTGTACA	GAAATGGTGA	TTTCTTTATT	1320
TCATCCAAAG	ATCTGGGCTA	TGACTATAGC	TATCTACAAG	ATTCAGACCC	AGACTCTTT	1380
CAAGACTACA	TTAAGTCCTA	TTTGGAACAA	GCGAGTCGGA	TCTGGTCATG	GCTCCTTGGG	1440
CGGGCGATGG	TAGGGGCCGT	CCTCACTGCC	CTGCTGGCAG	GGCTTGTGAG	CTTGTGTGT	1500
CGTCACAAGA	GAAAGCAGCT	TCCTGAAGAA	AAGCAGCCAC	TCCTCATGGA	GAAAGAGGAT	1560
TACCACAGCT	TGTATCAGAG	CCATTAA				1587

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1587 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATGCTCCTGG CTGTTTGTA CTGCCTGCTG TGGAGTTCC AGACCTCCGC TGGCCATTTC	60
CCTAGAGCCT GTGTCTCCTC TAAGAACCTG ATGGAGAAGG AATGCTGTCC ACCGTGGAGC	120
GGGGACAGGA GTCCCTGTGG CCAGCTTCA GGAGAGGTT CCTGTCAGAA TATCCTTCTG	180
TCCAATGCAC CACTTGGGCC TCAATTCCC TTCACAGGGG TGGATGACCG GGAGTCGTGG	240
CCTTCCGTCT TTTATAATAG GACCTGCCAG TGCTCTGGCA ACTTCATGGG ATTCAACTGT	300
GGAAACTGCA AGTTTGGCTT TTGGGGACCA AACTGCACAG AGAGACGACT CTTGGTGAGA	360
AGAAACATCT TCGATTTGAG TGCCCCAGAG AAGGACAAAT TTTTGCGCTA CCTCACTTTA	420
GCAAAGCATA CCATCAGCTC AGACTATGTC ATCCCCATAG GGACCTATGG CCAAATGAAA	480
AATGGATCAA CACCCATGTT TAACGACATC AATATTATG ACCTCTTGT CTGGATGCAT	540
TATTATGTGT CAATGGATGC ACTGCTTGGG GGATATGAAA TCTGGAGAGA CATTGATTTT	600
GCCCATGAAG CACCAGCTT TCTGCCTTGG CATAGACTCT TCTTGTGCG GTGGGAACAA	660
GAAATCCAGA AGCTGACAGG AGATGAAAAT TTCACTATTG CATATTGGGA CTGGCGGGAT	720
GCAGAAAAGT GTGACATTTG CACAGATGAG TACATGGAG GTCAGCACCC CACAAATCCT	780
AACTTACTCA GCCCAGCATC ATTCTTCTCC TCTTGGCAGA TTGTCTGTAG CCGATTGGAG	840
GAGTACAACA GCCATCAGTC TTTATGCAAT GGAACGCCCG AGGGACCTTT ACGGCGTAAT	900
CCTGGAAACC ATGACAAATC CAGAACCCCA AGGCTCCCT CTTCAGCTGA TGTAGAATT	960
TGCCTGAGTT TGACCCAATA TGAATCTGGT TCCATGGATA AAGCTGCCAA TTTCAGCTTT	1020
AGAAATACAC TGGAAGGATT TGCTAGTCCA CTTACTGGG TAGCGGATGC CTCTCAAAGC	1080
AGCATGCACA ATGCCTTGCA CATCTATATG AATGGAACAA TGTCCCAGGT ACAGGGATCT	1140
GCCAACGATC CTATCTTCCCT TCTTCACCAT GCATTTGTTG ACAGTATTT TGAGCAGTGG	1200
CTCCGAAGGC ACCGTCCTCT TCAAGAAGTT TATCCAGAAG CCAATGCACC CATTGGACAT	1260
AACCAGGAAT CCTACATGGT TCCTTTATA CCACTGTACA GAAATGGTGA TTTCTTTATT	1320
TCATCCAAAG ATCTGGGCTA TGACTATAGC TATCTACAAG ATTCAAGACCC AGACTCTTT	1380
CAAGACTACA TTAAGTCCTA TTTGGAACAA GCGAGTCGGA TCTGGTCATG GTCCTTGGG	1440

GCGGCGATGG TAGGGGCCGT CCTCACTGCC	CTGCTGGCAG GGCTTGTGAG CTTGCTGTGT	1500
CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC	TCCTCATGGA GAAAGAGGAT	1560
TACCACAGCT TGTATCAGAG CCATTAA		1587

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TAAATGGCTC TGATACAAGC T 21

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCAAGTTTGG CTTTTGGGGA 20

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATGCTCCTGG CTGTTTGTA CTG 23

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTCTGT A CAGTGGTATA AAAGGAACCA TGTAGGATT CCGGTTATGT CTAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTCTGT A CAGTGGTATA AAAGGAACCA TGTAGGATT CCGGTTATGT CCAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGTTGGCCAA TCTACTCCCC GG	22
--------------------------	----

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCTCACTCAG TGTGGCAAAG	20
-----------------------	----

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCACTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGGTCT GCCGTTACTG CCCTGTGGGG	180
CAAGGTGAAC GTGGATGAAG TTGGTGGTGA GGCCCTGGC AGGTTGGTAT CAAGGTTACA	240
AGACAGGTTT AAGGAGACCA ATAGAAACTG GGCATGTGGA GACAGAGAAG ACTCTTGGGT	300
TTCTGATAGG CACTGACTCT CTCTGCCTAT TGGTCTATTT TCCCACCCCTT AGGCTGCTGG	360
TGGTCTACCC TTGGACCCAG AGGTTCTTG AGTCCTTG GGATCTGTCC ACTCCTGATG	420
CTGTTATGGG CAACCCTAAG GTGAAGGCTC ATGGCAAGAA AGTGCTCGGT GCCTTAGTG	480
ATGGCCTGGC TCACCTGGAC AACCTCAAGG GCACCTTGCA CACACTGAGT GAGC	534

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTTGGCCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCACTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCT AGAGGTTCTT TGAGTCCTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCCTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 536 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGTTGGCCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGAGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCACTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCCTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 64 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAAUACUCAA GCUUGCAUGC CUGCAGGUCG ACUCUAGAGG AUCCCCGGGU ACCGAGCUCG 60  
AAUU 64

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GGCTGACAAG AAGGAAACTC 20

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCAGGCAGCG GCTAGGAGAG ATGGG 25

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60  
GAGGTACTGG GGAGGAGCCG GTCGGAAACG CCCACTCTCT TGATGTATAA ATATCACTGC 120  
ATTCGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTTC 180  
TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC 240  
CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC 300  
ATTTTAGAAG TAGGCCAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G 351

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCTGACAAG AAGGAAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG	60
GAGGAGCCGG TCGGGAACAC CCACHTTCTT GATGTATAAA TATCACTGCA TTTCGCTCTG	120
TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT	180
AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACTTAGCC AGTGCTGGC	240
AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT	300
AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG	340

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GGCTGACAAG AAGGAAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG	60
GAGGAGCCGG TCGGGAACAC CCACHTTCTT GGTGTATAAA TATCACTGCA TTTCGCTCTG	120
TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT	180
AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACTTGGCC AGTGCTGGC	240
AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT	300
AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG	340

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG	60
GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC	120
ATTCGCTCT GTATTCAAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGGTTC	180
TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC	240
CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC	300
ATTTTAGAAG TAGGCTAGTG TGTGTTCCA TCTCTCCTAG CCGCCGCCTG G	351

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GGCTGACAAG AAGGAAACTC GCTGAAACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG	60
GAGGTACTGG GAAGGAGCCG GTCGGGAACG CCCACTTTCT TGATGTATAA ATATCACTGC	120
ATTCGCTCT GTATTCAAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGGTTC	180
TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC	240
CGGTGCTGGG CAGAGTGAAT CCACGCTTGC TTGCTTAAAG CCCTCTTCAA TAAAGCTGCC	300
ATTTTAGAAG TAAGCTAGTG TGTGTTCCA TCTCTCCTAG CCGCCGCCTG G	351

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGA	60
GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC	120
ATTCGCTCT GTATTCAAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TAGGAGGGTTC	180
TCTCCAGCAC TAGCAGGTAG AGCCTGAGTG TTCCCTGCTA AACTCTCACC AGCACTTGGC	240
CGGTGCTGGG CAGAGCGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC	300
ATTTTAGAAG TAGGCTAGTG TGTGTTCCA TCTCTCCTAG CCGCCGCCTG G	351

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGTTGGCCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGAACCT	120
CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT AAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCACTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGTTGGCCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCACTGACT CTCTCTGCCT ATTAGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CACCGTCCTC TTCAAGAACG	TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTAT TTCATCCAAA	120	
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157	

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 833 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu			
1	5	10	15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys			
20	25	30	
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe			
35	40	45	
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile			
50	55	60	
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly			
65	70	75	80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln			
85	90	95	
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu			
100	105	110	
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys			
115	120	125	
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys			
130	135	140	
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu			
145	150	155	160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg			
165	170	175	

Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
180									185						190
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
195							200							205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
210						215							220		
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230				235				240		
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
				245				250						255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
				260				265				270			
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
				275				280				285			
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
				290				295				300			
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala
				305			310			315				320	
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala
				325				330				335			
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu
				340				345				350			
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu
				355				360				365			
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser
				370			375				380				
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr
				385			390			395				400	
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn
				405				410				415			
Leu	Trp	Gly	Arg	Leu	Glu	Gly	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	
				420				425				430			
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr
				435				440				445			
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val
				450				455			460				
Ala	Gly	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly
				465			470			475			480		
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe
				485				490				495			
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys
				500				505				510			

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 548 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Ala Cys Lys Leu Gly Thr Gly Arg Arg  
 530 535 540  
 Phe Thr Thr Ser  
 545

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 695 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300

Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala
305						310				315					320
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala
						325			330					335	
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu
					340			345						350	
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu
					355			360						365	
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser
					370			375						380	
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr
					385			390			395				400
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn
					405			410						415	
Leu	Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg
					420			425						430	
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr
					435			440						445	
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val
					450			455						460	
Ala	Gly	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly
					465			470			475				480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe
					485			490						495	
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys
					500			505						510	
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro
					515			520						525	
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser
					530			535						540	
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg
					545			550			555				560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser
					565			570						575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly
					580			585						590	
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Trp	Leu	Leu	Val	
					595			600						605	
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser
					610			615						620	
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His
					625			630			635				640

Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp
					645				650			655			
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr
		660					665				670				
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ser	His	Pro	Leu
		675				680				685					
Arg	Gly	Gly	Pro	Gly	Leu	His									
		690			695										

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 310 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10				15		
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
				20				25				30			
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
				35			40				45				
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50				55				60						
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70				75			80			
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85				90				95			
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
				100				105				110			
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
	115				120				125						
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130				135				140						
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
	145				150			155			160				
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165				170				175			
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
	180				185				190						
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
	195				200				205						

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ser Trp Arg Gly Cys Ile Pro Trp Pro Cys Pro  
 290 295 300  
 Trp Arg Trp Arg Trp Gly  
 305 310

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 322 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly  
 1 5 10 15  
 Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly  
 20 25 30  
 His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr  
 35 40 45  
 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
 50 55 60  
 Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp  
 65 70 75 80  
 Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala  
 85 90 95  
 Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile  
 100 105 110  
 Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly  
 115 120 125  
 Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys  
 130 135 140  
 Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln  
 145 150 155 160

Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly	Tyr	Leu	Ile
					165				170					175	
Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Asp	Gln	Trp
				180				185					190		
Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn	Leu	Pro	Gly
				195				200					205		
Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	Glu	Glu	Trp
			210				215					220			
Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	Lys	Pro	Ala
			225				230			235				240	
Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys	Leu	Ser	Trp
			245					250					255		
Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp	Phe	Ala
			260					265					270		
Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	Phe	Leu	Glu	Arg
			275					280					285		
Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	Glu	Ser	Pro
			290				295					300			
Lys	Ser	Trp	Arg	Gly	Cys	Ile	Pro	Trp	Pro	Cys	Pro	Trp	Arg	Trp	Arg
			305				310			315				320	
Trp	Gly														

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 528 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	Asp	Gly
1				5					10					15	
His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly	Leu	Thr	Thr
				20					25					30	
Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	Ser	Leu
				35				40					45		
Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	Val	Val	Phe	Asp
				50				55					60		
Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Tyr	Lys	Ala	
				65				70					80		
Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	Leu	Ile
				85					90				95		

Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly  
 100 105 110  
 Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys  
 115 120 125  
 Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln  
 130 135 140  
 Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile  
 145 150 155 160  
 Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp  
 165 170 175  
 Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly  
 180 185 190  
 Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp  
 195 200 205  
 Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala  
 210 215 220  
 Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp  
 225 230 235 240  
 Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala  
 245 250 255  
 Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg  
 260 265 270  
 Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro  
 275 280 285  
 Lys Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala  
 290 295 300  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 305 310 315 320  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 325 330 335  
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro  
 340 345 350  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 355 360 365  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 370 375 380  
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 385 390 395 400  
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val  
 405 410 415  
 Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg  
 420 425 430

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 435 440 445  
 Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
 450 455 460  
 Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His  
 465 470 475 480  
 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala  
 485 490 495  
 Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro  
 500 505 510  
 Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu  
 515 520 525

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 315 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly  
 1 5 10 15  
 Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly  
 20 25 30  
 His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr  
 35 40 45  
 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
 50 55 60  
 Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp  
 65 70 75 80  
 Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala  
 85 90 95  
 Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile  
 100 105 110  
 Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly  
 115 120 125  
 Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys  
 130 135 140  
 Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln  
 145 150 155 160

Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile  
 .165 170 175  
 Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp  
 180 185 190  
 Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly  
 195 200 205  
 Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp  
 210 215 220  
 Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala  
 225 230 235 240  
 Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp  
 245 250 255  
 Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala  
 260 265 270  
 Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg  
 275 280 285  
 Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro  
 290 295 300  
 Lys Ala Ala Leu Glu His His His His His His  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTCA	60
GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG	120
GATGATTGTA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA	180
GATGAAGCTC CCAGAACGCC AGAGGCTGCT CCCCCCGTGG CCCCTGCACC AGCAGCTCCT	240
ACACCGGCCGG CCCCTGCACC AGCCCCCTCC TGGCCCTGT CATCTTCTGT CCCTTCCCAG	300
AAAACCTACC AGGGCAGCTA CGGTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG	360
TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAAGATGT TTTGCCAACT GGCAAAGACC	420
TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCCG GCACCCGCGT CCGCGCCATG	480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCCTGCC CCACCATGAG	540
CGCTGCTCAG ATAGCGATGG TCTGGCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT	600

TTGCGTGTGG	AGTATTTGGA	TGACAGAAC	ACTTTGCAC	ATAGTGTGGT	GGTGCCTAT	660
GAGCCGCCTG	AGGTTGGCTC	TGACTGTACC	ACCATCCACT	ACAACTACAT	GTGTAACAGT	720
TCCTGCATGG	GCGGCATGAA	CCGGAGGCC	ATCCTCACCA	TCATCACACT	GGAAGACTCC	780
AGTGGTAATC	TACTGGGACG	GAACAGCTTT	GAGGTGCGTG	TTTGTGCCTG	TCCTGGGAGA	840
GACCGGCGCA	CAGAGGAAGA	GAATCTCCGC	AAGAAAGGGG	AGCCTCACCA	CGAGCTGCC	900
CCAGGGAGCA	CTAAGCGAGC	ACTGCCAAC	AACACCAGCT	CCTCTCCCCA	GCAAAGAAG	960
AAACCACTGG	ATGGAGAATA	TTTCACCCCTT	CAGATCCGTG	GGCGTGAGCG	CTTCGAGATG	1020
TTCCGAGAGC	TGAATGAGGC	CTTGGAACTC	AAGGATGCC	AGGCTGGGAA	GGAGCCAGGG	1080
GGGAGCAGGG	CTCACTCCAG	CCACCTGAAG	TCCAAAAGG	GTCAGTCTAC	CTCCGCCAT	1140
AAAAAACTCA	TGTTCAAGAC	AGAAGGGCCT	GACTCAGACT	GA		1182

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGGAGGAGC	CGCAGTCAGA	TCCTAGCGTC	GAGCCCCCTC	TGAGTCAGGA	AACATTTCA	60
GACCTATGGA	AACTACTTCC	TGAAAACAAC	GTTCTGTCCC	CCTTGCCTGC	CCAAGCAATG	120
GATGATTGGA	TGCTGTCCCC	GGACGATATT	GAACAATGGT	TCACTGAAGA	CCCAGGTCCA	180
GATGAAGCTC	CCAGAATGCC	AGAGGCTGCT	CCCCCGTGG	CCCCTGCACC	AGCAGCTCCT	240
ACACCGGCGG	CCCCTGCACC	AGCCCCCTCC	TGGCCCTGT	CATCTTCTGT	CCCTTCCCAG	300
AAAACCTACC	AGGGCAGCTA	CGGTTCCGT	CTGGGCTTCT	TGCATTCTGG	GACAGCCAAG	360
TCTGTGACTT	GCACGTACTC	CCCTGCCCTC	AAACAAGATGT	TTTGCCTA	GGCCAAGACC	420
TGCCCTGCGC	AGCTGTGGGT	TGATTCCACA	CCCCCGCCCG	GCACCCGCGT	CCGCGCCATG	480
GCCATCTACA	AGCAGTCACA	GCACATGACG	GAGGTTGTGA	GGCGCTGCC	CCACCATGAG	540
CGCTGCTCAG	ATAGCGATGG	TCTGGCCCT	CCTCAGCATC	TTATCCGAGT	GGAAGGAAAT	600
TTGCGTGTGG	AGTATTTGGA	TGACAGAAC	ACTTTGCAC	ATAGTGTGGT	GGTGCCTAT	660
GAGCCGCCTG	AGGTTGGCTC	TGACTGTACC	ACCATCCACT	ACAACTACAT	GTGTAACAGT	720
TCCTGCATGG	GCGGCATGAA	CCGGAGGCC	ATCCTCACCA	TCATCACACT	GGAAGACTCC	780
AGTGGTAATC	TACTGGGACG	GAACAGCTTT	GAGGTGCGTG	TTTGTGCCTG	TCCTGGGAGA	840
GACCGGCGCA	CAGAGGAAGA	GAATCTCCGC	AAGAAAGGGG	AGCCTCACCA	CGAGCTGCC	900

CCAGGGAGCA CTAAGCGAGC ACTGCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG	960
AAACCACTGG ATGGAGAATA TTTCACCCCTT CAGATCCGTG GGC GTGAGCG CTTCGAGATG	1020
TTCCGAGAGC TGAATGAGGC CTTGGAACTC AAGGATGCC AGGCTGGAA GGAGCCAGGG	1080
GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAGG GTCAGTCTAC CTCCGCCAT	1140
AAAAAACTCA TGTTCAAGAC AGAAGGGCCT GACTCAGACT GA	1182

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTCA	60
GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG	120
GATGATTGGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA	180
GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCCGTGG CCCCTGCACC AGCAGCTCCT	240
ACACCCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCCTGT CATCTTCTGT CCCTTCCCAG	300
AAAACCTACC AGGGCAGCTA CGGTTCCGT CTGGGCTTCT TGCAATTCTGG GACAGCCAAG	360
TCTGTGACTT GCACGTACTC CCCTGCCCTC ACAAGAGATGT TTTGCCAACT GGCAAGACC	420
TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCCG GCACCCGCGT CCGCGCCATG	480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCGCTGCC CCACCATGAG	540
CGCTGCTCAG ATAGCGATGG TCTGGCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT	600
TTGCGTGTGG AGTATTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT	660
GAGCCGCCTG AGGTTGGCTC TGACTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT	720
TCCTGCATGG GCGGCATGAA CCGGAGACCC ATCCTCACCA TCATCACACT GGAAGACTCC	780
AGTGGTAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCCTG TCCTGGGAGA	840
GACCCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCC	900
CCAGGGAGCA CTAAGCGAGC ACTGCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG	960
AAACCACTGG ATGGAGAATA TTTCACCCCTT CAGATCCGTG GGC GTGAGCG CTTCGAGATG	1020
TTCCGAGAGC TGAATGAGGC CTTGGAACTC AAGGATGCC AGGCTGGAA GGAGCCAGGG	1080
GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAGG GTCAGTCTAC CTCCGCCAT	1140
AAAAAACTCA TGTTCAAGAC AGAAGGGCCT GACTCAGACT GA	1182

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCTGGGCTTC TTGCATTCTG

20

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGGGCAGT GCTCGCTTAG

20

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACATACA TGTGTAACAG TTCCTGCATG GGCAGGCATGA ACCGGAGGCC	420
CATCCTCAC C ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGGTGCCT GTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCAC C ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
CGGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTC CGTCCCAGTA GATTACACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCAGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTCCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCCGG ACAGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAACCCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGACAGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGCG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCCGC GGCACCCCGCG TCCCGGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGCC	240
TCCTCAGCAT CTTATCCGAG TGGAAAGGAAA TTTGCGTGTG GAGTATTGAG ATGACAGAAA	300
CACTTTCGA CATAGTGTGG TGGTGCCTA TGAGCCGCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACATACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC	420
CATCCTCACC ATCATCACAC TGGAAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480

TGAGGTGCGT GTTTGTGCCT GTCCTGGAG AGACCGGCCG ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCAC CACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GC GGAGATT C TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTT CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCGCAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGACAGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAAGGAAA TTTGCGTGTG GAGTATTGAG ATGACAGAAA	300

CACTTTCGA CATA GTGTGG TGGTGCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACA AACTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGACC	420
CATCCTCACCA ATCATCACAC TGGAAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCGT GTTTGTGCCT GTCCTGGAG AGACCGGCGC ACAGAGGAAG AGAACATCTCCG	540
CAAGAAAGGG GAGCCTCACCA ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GCGGAGATTC TCTTCCTCTG TGGGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTG CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGTCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGGGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCCCTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GAGGATGGGA CTCCGGTTCA TG	22
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(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CATGAACCGG AGTCCCCATCC TCAC

24

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCACAAACAT GCACCTCAAA GCT

23

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CAGCTTGAG GTGCATGTTT GT

22

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240

TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTGG ATGACAGAAA	300
CACTTTCGA CATACTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACCTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGTCC	420
CATCCTCACCC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCGT GTTGTGCCT GTCCTGGAG AGACCGGCAG ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACCC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTG CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGACTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTCCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGAAA ACATCTTGT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCCTGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTCGA CATAGTGTGG TGGTGCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAAC TACA TGTGTAACAG TTCCCTGCATG GGCAGGCATGA ACCGGAGGCC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCAT GTTGTGCCT GTCCTGGAG AGACCGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
CGGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CATGCACCTC	120
AAAGCTGTTG CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGGGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAACGCA AGAAGCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 427 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTGAG ATGACAGAAA	300
CACTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTAACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGTCC	420
CATCCTC	427

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATGAACCGG AGTCCCATCC TCACCACAT CACACTGGAA GACTCCAGTG GTAATCTACT	60
GGGACGGAAC AGCTTGAGG TGCCTGTTG TGCCTGTCCT GGGAGAGACC GGCGCACAGA	120
GGAAGAGAAC CTCCGCAAGA AAGGGGAGCC TCACCACGAG CTGCCCCAG GGAGCACTAA	180
GCGAGCACTG CCCAAC	196

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 498 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCCG TCCCGGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAAC TACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC	420
CATCCTCACC ATCATCACAC TGGAAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCAT GTTTGTGC	498

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CAGCTTGAG GTGCATGTTT GTGCCGTGCC TGGGAGAGAC CGGCGCACAG AGGAAGAGAA	60
TCTCCGCAAG AAAGGGGAGC CTCACCACGA GCTGCCCTA GGGAGCACTA AGCGAGCACT	120
GCCCAAC	127

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GGTTTTCTT TGAGGTTTAG	20
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(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GCGACACTCC ACCATAGAT

19

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CTGTCTTCAC GCAGAAAGC

19

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCACGGTCTA CGAGACCTC

19

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GATCTACTAG TCATATGGAT

20

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TCGGTACCCG GGGATCCGAT

20

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCTG CAGCCTCCAG	60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC	180
CCCGCAAGAC TGCTAGCCGA GTAGTGTGG GTCGCAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCCTG CGAGTGCCCG GGGAGGTCTC GTAGACCGTG C	281

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCTG CAGCCTCCAG	60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGACTGTC TTCACCGAGA	120
AAGCGTCTAG CCATGGCGTT AGTATGAGTG TCGTGCAGCC TCCAGGACCC CCCCTCCCGG	180
GAGAGCCATA GTGGTCTGCG GAACCGGTGA GTACACCGGA ATTGCCAGGA CGACCGGGTC	240
CTTTCTTGGT TCAACCCGCT CAATGCCTGG AGATTTGGC GTGCCCGCG AAGACTGCTA	300
GCCGAGTAGT GTTGGGTCGC GAAAGGCCTT GTGGTACTGC CTGATAGGGT GCTTGCAGT	360
GCCCCGGGAG GTCTCGTAGA CCGTGC	386

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTG CAGCCTCCAG	60
GCCCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC	180
CCCGCGAGAC TGCTAGCCGA GTAGTGTGG GTCGCGAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCTTG CGAGTGCCCG GGGAGGTCTC GTAGACCGTG C	281

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTG CAGCCTCCAG	60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC GTGGATGTAA CCCGCTCAAT GCCTGGAGAT TTGGGCGTGC	180
CCCCGCAAGA CTGCTAGCCG AGTAGTGTGG GGTCGCGAAA GGCTTGTGG TACTGCCTGA	240
TAGGGTGCTT GCGAGTGCCCG CGGGAGGTCTC CGTAGACCGTG GC	282

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTG CAGCCTCCAG	60
GCCCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CGGGAAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG CCCGGCCATT TGGGCGTGCC	180
CCCGCAAGAC TGCTAGCCGA GTAGCGTTGG GTTGCAGAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCTTG CGAGTACCCCC GGGAGGTCTC GTAGACCGTG C	281

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTGTCTTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAC GAGTGTCTGT CAGCCTCCAG	60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CGGAATCGC	120
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA CCCAGAAATT TGGGCCTGCC	180
CCCGCGAGAT CACTAGCCGA GTAGTGTGG GTCGCAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C	281

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAGGCACCC TATCAGGCAG TACCACAAGG	60
CCTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCAG GGGCACGCC AAATCTCCAG	120
GCATTGAGCG GGTATCCA AGAAAGGACC CGGTCGCCT GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT	240
CATACTAACG CCATGGCCAG ACGCTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCAGG GGGCACGCC AAATCTCCAG	120
GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCCCT GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCAGG GGGCACGCC AAATCTCCAG	120
GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCCCT GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCAGG GGGCACGCC AAATCTCCAG	120
GCATTGAGCG GGTTACATCC ACGAAAGGAC CGGGTCGTCC TGGCAATTCC GGTGTACTCA	180
CCGGTTCCGC AGACCACTAT GGCTCTCCCG GGAGGGGGGG TCCTGGAGGC TGCACGACAC	240
TCATACTAAC GCCATGGCTA GACGCTTCTG GCGTGAAGAC AG	282

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCACGGTCTA CGAGACCTCC CGGGGTACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTCGCAA CCCAACGCTA CTCGGCTAGC AGTCTTGCAG GGGCACGCC AAATGGCCGG	120
GCATAGAGTG GGTTTATCCA AGAAAGGACC CAGTCTCCC GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCGG GAGGGGGGG CCTGGAGGCT GTACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCACGGTCTA CGAGACCTCC CGGGGCCTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTCGCGA CCCAACACTA CTCGGCTAGT GATCTCGAGG GGGCACGCC AAATTCTGG	120
GTATTGAGCG GGTTGCTCCA AGAAAGGACC CGGTCACCCC AGCGATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCGG GAGGGGGGT CCTGGAGGCT GCACGACACT	240
CGTACTAACG CCATGGCTAG GCGCTTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ATCAACATCC GGCGGGTGGT

20

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GGGGCCTCGC TACGGACCAAG

20

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATCAACATCC GGCGGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC	60
CAATTCATGG ACCAGAACAA CCCGCTGTCTG GGGTTGACCC ACAAGCGCCG ACTGTCGGCG	120
CTGGGGCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG	180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC	240
GGCTCGCTGT CGGTGTACGC GCAGGTCAAC CCGTTGGGT TCATCGAAAC GCCGTACCGC	300
AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC	360
CGCCACGTGG TGGCACAGGC CAATTGCGCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG	420
CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC	480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG	540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG	600
CTGGTCCCGTA GCGAGGCCCG	620

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

ATCAACATCC GGCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC	60
CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCT ACAAGCGCCG ACTGTCGGCG	120
CTGGGGCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG	180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC	240
GGCTCGCTGT CGGTGTACGC GCAGGTCAAC CCGTTGGGT TCATCGAAAC GCCGTACCGC	300
AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC	360
CGCCACGTGG TGGCACAGGC CAATTGCGCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG	420
CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC	480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG	540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG	600
CTGGTCCGTA GCGAGGCCCC	620

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ATCAACATCC GGCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC	60
CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCC ACAAGCGCCG ACTGTTGGCG	120
CTGGGGCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG	180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC	240
GGCTCGCTGT CGGTGTACGC GCAGGTCAAC CCGTTGGGT TCATCGAAAC GCCGTACCGC	300
AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC	360
CGCCACGTGG TGGCACAGGC CAATTGCGCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG	420
CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC	480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG	540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG	600
CTGGTCCGTA GCGAGGCCCC	620

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG	120
CAGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCGCC	180
TTGCGGCGGA CCAGCACCGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA	300
ACACACCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGCAG CGGGTGCACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT	480
GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCGCTTGT GGGTCAACCC CGACAGCGGG	540
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGCG	600
ACACACGGCC GGATGTTGAT	620

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG	120
CAGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCGCC	180
TTGCGGCGGA CCAGCACCGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA	300
ACACACCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGCAG CGGGTGCACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT	480

GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCGCTTGT AGGTCAACCC CGACAGCGGG	540
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAAACTCCTT GATCGCGGCG	600
ACCACCGGCC GGATGTTGAT	620

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GGGCCTCGC TACGGACAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG	120
CGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCGCC	180
TTGCGGCGGA CCAGCACCGC CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA	300
ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGCAGA CGGGTGCACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT	480
GACAGACCGC CGGGCCCCAG CGCCAACAGT CGGCGCTTGT GGGTCAACCC CGACAGCGGG	540
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAAACTCCTT GATCGCGGCG	600
ACCACCGGCC GGATGTTGAT	620

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AGCTCGTATG GCACCGGAAC	20
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(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTGACCTCCC ACCCGACTTG

20

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AGCTCGTATG GCACCGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCCTGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTGCGTGGCT GGAACACCCC	300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTCGA CCGCATGGGC GGCGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

AGCTCGTATG GCACCGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCCTGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTGCGTGGCT GGAACACCCC	300

GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTCGA CCGCATGGC GGCGGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTECC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC	300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTCGA CCGCATGGC GGCGGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCCTGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCACATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTGCGTGGCT GGAACACCCC	300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGTTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGC GGCGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCG	60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCCGGAT CTGGCTTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGAACCGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCTTGGCG	300
AACTCGTCGG CCAATTCCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTCGTGCG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATACTGAGCT	620

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCTTGGCG	300
AACTCGTCGG CCAATTCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTCGTCTG GGGTGTTCGT CCATACGACC TCGATGCCGG TGTTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATACTGAGCT	620

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCTTGGCG	300
AACTCGTCGG CCAATTCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480

GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTCGTCG GGGTGTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATAcgAGCT	620

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCTTGGCG	300
AACTCGTCGG CCAATTCCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCCTC GGCACCGGCCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTCGTCG GGGTGTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATAcgAGCT	620

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGAGTTTGAT CCTGGCTCAG	20
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(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGCGGACGGG TGAGTAA

17

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CTGCTGCCTC CCGTAGGAGT

20

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGACGTCAA GTCATCATGG CCCTTACGA

29

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTACAAGGCC CGGGAACGTA TTCACCG

27

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GCAACGAGCG CAACCC

16

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ATGACGTCAA GTCATCATGG CCCTTA

26

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1542 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA	60
GTCGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGCGGAC GGGTGAGTAA	120
TGTCTGGAA ACTGCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT	180
AACGTCGCAA GACCAAAGAG GGGGACCTTC GGGCCTCTTG CCATCGGATG TGCCCAGATG	240
GGATTAGCTA GTAGGTGGGG TAACGGCTCA CCTAGGCGAC GATCCCTAGC TGGTCTGAGA	300
GGATGACCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG	360
GGAATATTGC ACAATGGCG CAAGCCTGAT GCAGCCATGC CGCGTGTATG AAGAAGGCCT	420
TCGGTTGTA AAGTACTTTC AGCGGGGAGG AAGGGAGTAA AGTTAATACC TTTGCTCATT	480
GACGTTACCC GCAGAAGAAG CACCGGCTAA CTCCGTGCCA GCAGCCGCGG TAATACGGAG	540
GGTGCAAGCG TTAATCGGAA TTACTGGCG TAAAGCGCAC GCAGGCGGTT TGTAAAGTCA	600
GATGTGAAAT CCCCAGGCTC AACCTGGAA CTGCATCTGA TACTGGCAAG CTTGAGTCTC	660
GTAGAGGGGG GTAGAATTCC AGGTGTAGCG GTGAAATGCG TAGAGATCTG GAGGAATACC	720
GGTGGCGAAG GCGGCCCT GGACGAAGAC TGACGCTCAG GTGCGAAAGC GTGGGGAGCA	780
AACAGGATTA GATACTCTGG TAGTCCACGC CGTAAACGAT GTCGACTTGG AGGTTGTGCC	840
CTTGAGGCCTG GGCTTCCGGA GCTAACGCGT TAAGTCGACC GCCTGGGGAG TACGGCCGCA	900
AGGTAAAAC TCAAATGAAT TGACGGGGC CCGCACAAGC GGTGGAGCAT GTGGTTAAC	960
TCGATGCAAC GCGAAGAACCC TTACCTGGTC TTGACATCCA CGGAAGTTTT CAGAGATGAG	1020
AATGTGCCTT CGGGAACCGT GAGACAGGTG CTGCATGGCT GTCGTCAGCT CGTGTGTGA	1080

AATGTTGGGT	TAAGTCCCGC	AACGAGCGCA	ACCCTTATCC	TTTGTGCCA	GCGGTCCGGC	1140
CGGGAACTCA	AAGGAGACTG	CCAGTGATAA	ACTGGAGGAA	GGTGGGGATG	ACGTCAAGTC	1200
ATCATGGCCC	TTACGACCAG	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAACG	1260
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC	1320
TCGACTCCAT	GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT	1380
TCCCAGGCT	TGTACACACC	GCCCCTCACA	CCATGGGAGT	GGGTTGCAAA	AGAAGTAGGT	1440
AGCTTAACCT	TCGGGAGGGC	GCTTACCACT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA	1500
CAAGGTAACC	GTAGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA		1542

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1513 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

TTTTTATGGA	GAGTTTGATC	CTGGCTCAGA	GTGAACGCTG	GCGGCGTGCC	TAATACATGC	60
AAGTCGAACG	ATGAAGCTTC	TAGCTTGCTA	GAAGTGGATT	AGTGGCGCAC	GGGTGAGTAA	120
GGTATAGTTA	ATCTGCCCTA	CACAAGAGGA	CAACAGTTGG	AAACGACTGC	TAATACTCTA	180
TACTCCTGCT	TAACACAACT	TGAGTAGGGA	AAGTTTTCG	TGTTAGGATG	AGACTATATA	240
GTATCAGCTA	GTTGGTAAGG	TAATGGCTTA	CCAAGGCTAT	GACGCTTAAC	TGGTCTGAGA	300
GGATGATCAG	TCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTAG	360
GGAATATTGC	GCAATGGGGG	AAACCCTGAC	GCAGCAACGC	CGCGTGGAGG	ATGACACTTT	420
TCGGAGCGTA	AACTCCTTT	CTTAGGGAAG	AATTCTGACG	GTACCTAAGG	AATAAGCACC	480
GGCTAACTCC	GTGCCAGCAG	CCGCGGTAAAT	ACGGAGGGTG	CAAGCGTTAC	TCGGAATCAC	540
TGGCGTAAA	GGGCGCGTAG	GCGGATTATC	AAGTCTCTTG	TGAAATCTAA	TGGCTTAACC	600
ATTAAACTGC	TTGGGAAACT	GATAGTCTAG	AGTGAGGGAG	AGGCAGATGG	AATTGGTGGT	660
GTAGGGTAA	AATCCGTAGA	TATCACCAAG	AATACCCATT	GCAGAACGCGA	TCTGCTGGAA	720
CTCAACTGAC	GCTAAGGCAC	GAAAGCGTGG	GGAGCAAACA	GGATTAGATA	CCCTGGTAGT	780
CCACGCCCTA	AACGATGTAC	ACTAGTTGTT	GGGGTGCTAG	TCATCTCAGT	AATGCAGCTA	840
ACGCATTAAG	TGTACCGCCT	GGGGAGTACG	GTGCGAAGAT	TAAAACTCAA	AGGAATAGAC	900
GGGGACCCGC	ACAAGCGGTG	GAGCATGTGG	TTTAATTGGA	AGATACGCGA	AGAACCTTAC	960
CTGGGCTTGA	TATCCTAAGA	ACCTTTAGA	GATAAGAGGG	TGCTAGCTTG	CTAGAACCTTA	1020

GAGACAGGTG	CTGCACGGCT	GTCGTCAGCT	CGTGTGCGTGA	GATGTTGGGT	TAAGTCCC	GC	1080
AACGAGCGCA	ACCCACGTAT	TTAGTTGCTA	ACGGTTCGGC	CGAGCACTCT	AAATAGACTG		1140
CCTTCGTAAG	GAGGAGGAAG	GTGTGGACGA	CGTCAAGTCA	TCATGGCCCT	TATGCCAGG		1200
GCGACACACG	TGCTACAATG	GCATATAGAA	TGAGACGCAA	TACCGCGAGG	TGGAGCAAAT		1260
CTATAAAATA	TGTCCCAGTT	CGGATTGTT	TCTGCAACTC	GAGAGCATGA	AGCCGGAATC		1320
GCTAGTAATC	GTAGATCAGC	CATGCTACGG	TGAATACGTT	CCCGGGTCTT	GTACTCACCG		1380
CCCGTCACAC	CATGGGAGTT	GATTCACTC	GAAGCCGGAA	TACTAAACTA	GTTACCGTCC		1440
ACAGTGGAAT	CAGCGACTGG	GGTGAAGTCG	TAACAAGGTA	ACCGTAGGAG	AACCTGCGGT		1500
TGGATCACCT	CCT						1513

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1555 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

TTTTATGGAG	AGTTTGATCC	TGGCTCAGGA	TGAACGCTGG	CGCGTGCCT	AATACATGCA		60
AGTCGAGCGA	ACGGACGAGA	AGCTTGCTTC	TCTGATGTTA	GGCGCGGAGC	GGTGAGTAAC		120
ACGTGGATAA	CCTACCTATA	AGACTGGGAT	AACTTCGGGA	AACCGGAGCT	AATACCGGAT		180
AATATTTGA	ACCGCATGGT	TCAAAAGTGA	AAGACGGTCT	TGCTGTCACT	TATAGATGGA		240
TCCCGCCTGC	ATTAGCTAGT	TGGTAAGGTA	ACGGCTTACC	AAGGCAACGA	TACGTAGCCG		300
ACCTGAGAGG	GTGATCGGCC	ACACTGGAAC	TGAGACACGG	TCCAGACTCC	TACGGGAGGC		360
AGCAGTAGGG	AATCTTCCGC	AATGGGCGAA	AGCCTGACGG	AGCAACGCCG	CGTGAGTGAT		420
GAAGGTCTTC	GGATCGTAAA	ACTCTGTTAT	TAGGGAAGAA	CATATGTGTA	AGTAACTGTG		480
CACATCTTGA	CGGTACCTAA	TCAGAAAGCC	ACGGCTAACT	ACGTGCCAGC	AGCCGCGGTA		540
ATACGTAGGT	GGCAAGCGTT	ATCCGGAATT	ATTGGGCGTA	AAGCGCGCGT	AGGCGGTTTT		600
TTAAGTCTGA	TGTGAAAGCC	CACGGCTCAA	CCGTGGAGGG	TCATTGGAAA	CTGGAAAACT		660
TGAGTGCAGA	AGAGGAAAGT	GGAATTCCAT	GTGTAGCGGT	GAAATGCGCA	GAGATATGGA		720
GGAACACCAG	TGGCGAAGGC	GACTTCTGG	TCTGTAACTG	ACGCTGATGT	GCGAAAGCGT		780
GGGGATCAA	CAGGATTAGA	TACCCTGGTA	GTCCACGCCG	TAACAGATGA	GTGCTAAGTG		840
TTAGGGGGTT	TCCGCCCTT	AGTGCTGCAG	CTAACGCATT	AAGCACTCCG	CCTGGGGAGT		900
ACGACCGCAA	GGTTGAAACT	CAAAGGAATT	GACGGGGACC	CGCACAGCG	GTGGAGCATG		960

TGGTTAATT CGAAGCAACG CGAAGAACCT TACCAAATCT TGACATCCTT TGACAACCTCT	1020
AGAGATAGAG CCTTCCCTT CGGGGGACAA AGTGACAGGT GGTGCATGGT TGTCGTCAGC	1080
TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCCTTAAG CTTAGTTGCC	1140
ATCATTAAGT TGGGCACTCT AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG	1200
ACGTCAAATC ATCATGCCCT TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA	1260
AAGGGCAGCG AAACCGCGAG GTCAAGCAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT	1320
AGTCTGCAAC TCGACTACAT GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG	1380
GTGAATACGT TCCCAGGTAT TGTACACACC GCCCGTCACA CCACGAGAGT TTGTAACACC	1440
CGAAGCCGGT GGAGTAACCT TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG	1500
TGAAGTCGTA ACAAGGTAGC CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCT	1555

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 46 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GAAUACUCAA GCUUGCAUGC CUGCAGGUCG ACUCUAGAGG AUCCCC

.46

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 141 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

TTGACAATTA ATCATCGGCT CGTATAATGT GTGGAATTGT GAGCGGATAA CAATTCACA	60
CAGGAAACAG CGATGAATTC GAGCTCGGTA CCCGGGGATC CTCTAGAGTC GACCTGCAGG	120
CATGCAAGCT TGGCACTGGC C	141

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 144 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG AGACCACAAC GGTTCCCTC	60
TAGAAAATAAT TTTGTTAAC TTTAAGAAGG AGATATACAT ATGGCTAGCA TGACTGGTGG	120
ACAGCAAATG GGTCGGATCC GGCT	144

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TAATACGACT CACTATAGGG AGACCGGAAT TCGAATTCCG TGTATTCTAT AGTGTACCT	60
AAATCGAATT C	71

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 228 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60
CACTATAGGG CGAATTGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180
TTTCCTGTGT GAAATTGTTA TCCGCTCACCA ATTCCACACAC ACATACGA	228